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Human beta-amyloid
Beta-amyloid pepti
Human APP derived
Human APP derived
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Human beta-amyloid
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                                                                                                        2002, 13:56:34 ; Search time 33.8462 Seconds (without alignments) 39.370 Million cell updates/sec
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Beta-amyloid f
Beta-amyloid f
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAY39233
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ABB07973
AAW45343
AAY39236
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ABB07970
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AAB46235
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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57
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Match Length
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Maximum DB
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96US-0625765 97WO-US04966

28-MAR-1997; 29-MAR-1996;

09-0CT-1997

Gilchrest BA, Yaar M; WPI; 1997-512306/47.

(UYBO-) UNIV BOSTON

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Synthetic amyloid
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                                   Human amyloidogeni
                                                                                                                                       Synthetic amyloid
                                                                                                                                            Human Receptor to
Human APP derived
                                                                                                                                                                                                                                  Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment; neurotrophin receptor p75; p75NTR; nerve growth factor; NGF.
                                                                                                                                                                                                                         Peptide used for diagnosing and treating Alzheimer's disease.
                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                  1..10
/note= "disulphide bond"
                           AAB91832
AAW47229
AAY33408
                                                AAB84430
AAW81469
AAU93990
                                                                            AAW89357
AAW89360
AAW89361
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AAB91830
ABB05164
AAW81471
AAR60362
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AAR60363
AAY25134
AAW81472
AAY52132
                  AAB91815
AAB91805
                                        AAB84431
AAY33409
                                                                   AAW47228
AAW89356
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AAB91799
                                                               AAW02336
         AAB91782
                                                                                                                                                     AAR60364
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                             AAW45346 standard; peptide; 10 AA.
(first entry)
Disulfide-bond
                                                                                                                                                                                                               08-MAY-1998
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                                                                                                                                                                                                                                                                               WO9737228-A1
Synthetic.
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The invention relates to methods of therapy for Alzheimer's disease using peptides (AAM45343-6) that bind to the neurotrophin receptor p75 nerve growth factor receptor (NGFR) and competitively inhibit the binding of a beta-amyloid to the p75 NGFR. Also described is a new method for evaluating the risk of an individual to develop Alzheimer's disease using cultured neural crest-derived melanocytes. The methods can be used using cultured neural crest-derived melanocytes. The methods can be used neurodegenerative diseases mediated by beta-amyloid protein, or by aberrant activation of the low affinity NGFR localised on neural cell surfaces, such as autoimmune encephalomyelitis, Huntington's disease, cortico-basal degeneration, progressive supra-nuclear palsy, Gerotuan-Shausslesr Scheinker syndrome, Neimann-pick disease, and genoresive supranuclear palsy. In the diagnostic tests, the human melanocytes, which are easily obtainable from skin biopsies, are good model cells for the study and diagnosis of Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor; NGF; melanocyte; kerathnocyte; apoptosis; Bc1-2; beta-amyloid; Alzheimer's disease; pseudo-ligand; hair growth; hair colour; skin colour; alopecia areata; male pattern baldness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
/note= "C-terminus is attached via a peptide bond to
the N-terminus amino acid at position 1"
                Evaluating risk of individual to develop Alzheimer's - uses cultured epidermal melanocyte(s), also useful for developing therapies for neuro-degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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the C-terminus amino acid at position 10"
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                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 57; DB 18;
100.0%; Pred. No. 0.0012;
ive 0; Mismatches 0;
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                                                                                Claim 14; Page 21; 42pp; English.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
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Modified-site
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This sequence is a cyclic peptide which competes with and competitively inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR). P75NTR is a low affinity nerve growth factor (NGF) receptor which is expressed by melanocytes and keratinocytes of the basal epidermis. Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2 protein. If the receptor is occupied by appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other examples of appropriate ligands include this cyclic peptide. This peptide is based on the sequence of the binding fragment of beta-amyloid, which binds to p75NTR in Alzaheimer's disease. This cyclic peptide can be used in methods involve using this peptide or peptides AAY39234-Y39235 to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting apoptosis. The new method can induce or maintain hair growth, hair colour or skin colour. Inducing or maintaining hair growth is useful for treating alopecia areata or male pattern baldness in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibition of beta-amyloid binding to the p75 nerve growth factor receptor using polypeptides, useful in the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Controlling or manipulating melanocyte and keratinocyte cell death, useful for treating, e.g. alopecia areata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p75 nerve growth factor receptor; inhibitor; Alzheimer's disease; neurodegenerative disease; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //ote- "the peptide has a cyclic structure as a
result of the bonding between the two
cysteine residues"
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 57; DB 20;
100.0%; Pred. No. 0.0012;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta-amyloid-derived cyclic peptide #2.
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                                                67pp; English.
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97WO-US04966.
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Les 10; Conservative
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                                                4; Page 39;
                                                                                                                                                                                                                                                                                                                                                                    10 AA;
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The invention relates to methods for inhibiting binding of beta-amyloid to the p75 nerve growth factor receptor. The methods comprise contacting the cell with a substance that binds to the p75 nerve growth centacting the cell with a substance that binds to the p75 nerve growth can be proved to the p75 nerve growth can be present a citivation of the low affinity of by beta-amyloid protein, or by aberrant activation of the low affinity nerve growth factor receptor localised on neural cell surfaces. Such diseases include autoimmune encephalomyelitis, Huntington's disease, pick's disease, corticobasal degeneration, progressive supranuclear palsy, Gerotman-Shausslear Scheinker syndrome, Nieman-Pick disease and Down's syndrome. The present sequence is a cyclic peptide comprising a fragment of the human beta-amyloid protein to which a cysteine residue has been added at each end. The peptide inhibits binding of beta-amyloid to the p75 nerve growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic; Alzheimer's disease; neurotrophin receptor; NTR; human; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluating risk of an individual to develop Alzheimer's disease using cultured neural crest-derived melanocytes and methods of therapy for Alzheimer's disease using peptides that bind to the neurotrophin
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                               Claim 2; Column 18; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB07973 standard; peptide; 10 AA.
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96US-0625765.
97WO-US04966.
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e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
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28-MAR-1997;
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The invention relates to a method of inhibiting beta-amyloid binding to

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                      Involves contacting the cell with a substance having the amino acid sequence lysine-glycine-lysine or lysine-glycine-alanine. The substance binds to the p75 NGFR resulting in the inhibition of beta-amyloid protein or beta-amyloid peptide binding to the p75 NGFR. The invention is useful for evaluating the risk of an individual to develop Alzheimer's disease and methods of therapy for Alzheimer's disease using peptides that bind to the neurotrophin receptor (NTR) and competitively inhibit the binding of beta-amyloid to the receptor. In vitro methods are also provided for decreasing cell apoptosis mediated by beta-amyloid. The present sequence represents a cyclic peptide that competes for p75NTR binding with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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p75 nerve growth factor receptor (NGFR) of a cell. The method
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100.0%; Pred. No. 0.0012;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW45343 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US04966
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                                                                                                                                                                                                                                                                                                                                                                                                                           the beta-amyloid peptide
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Best Local Similarity
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Length

Query Match

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This sequence is amino acids 24-31 of beta-amyloid. This sequence can be used to generate cyclic peptide AAY99233. The cyclic peptide competes with and competitively inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75MTR) beta-amyloid binding to the p75 neurotrophin receptor which is expressed by melanocytes and keratinocytes of the basal epidemia. Apoptosis can be inhibited by p75MTR via the upregulation of the Bcl-2 protein. If the receptor is occupied by appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other cxamples of appropriate ligands include this cyclic peptide. This peptide is based on the sequence of the binding fragment of beta-amyloid, which binds to p75MTR in Alzheimer's disease. This cyclic peptide can be used in methods to control or manipulate keratinocyte or melanocyte cell death. The methods involve using this peptide or peptides AAY39234-Y3935 to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting a proportier. Inducing or maintening hair growth is useful for reating alopecia areata or mainten baldness in vertebrates.
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                             progressive supra-nuclear palsy, Gerotman-Shausslesr Scheinker syndrome, Neimann-Pick disease, and progressive supranuclear palsy. In the diagnostic tests, the human melanocytes, which are easily obtainable from skin biopsies, are good model cells for the study and diagnosis of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p75NTR; p75 neurotrophin receptor; nerve growth factor; NGF; melanocyte; keratinocyte; apoptosis; Bc1-2; beta-amyloid fragment; Alzheimer's disease; pseudo-ligand; hair growth; hair colour; skin colour; alopecia areata; male pattern baldness.
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cortico-basal degeneration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-amyloid fragment for generation of p75NTR inhibiting peptides
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                                                                                                                                                                                                                                                                                                          68.4%; Score 39; DB 18; I
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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encephalomyelitis, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 15; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                           8 AA;
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                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibition of beta-amyloid binding to the p75 nerve growth factor receptor using polypeptides, useful in the diagnosis and treatment of e.g. Alzheimer's disease
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                               Gaps
                                                                                                                                                                                                                                                                                Human; beta-amyloid; 'nootropic; neuroprotective; anticonvulsant; p75 nerve growth factor receptor; inhibitor; Alzheimer's disease; neurodegenerative disease.
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                             Indels
DB 20; L
68.4%; Score 39; DB
100.0%; Pred. No. 7.8
ive 0; Mismatches
                                                                                                                                                                AAG64001 standard; peptide; 8 AA.
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97WO-US04966
                                                                                                                                                                                                                                                       Human beta-amyloid peptide.
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                               Conservative
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Best Local Similarity
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Matches 8; Conserv
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                                                           2 VGSNKGAI 9
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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28-MAR-1997;
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                                                                                                                                    RESULT 7
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Schenk DB,
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                                                                                                                                                                                                         Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evaluating risk of an individual to develop Alzheimer's disease using cultured neural crest-derived melanocytes and methods of therapy for Alzheimer's disease using peptides that bind to the neurotrophin
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                                                                                                                                                                                                                               Alzheimer's disease; neurotrophin receptor; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%; Score 39; DB 23; I 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                 Beta-amyloid peptide fragment (residues 24-31).
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                                     ABB07970 standard; peptide; 8 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0163095.
96US-0625765.
97WO-US04966.
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nes 8; Conserv
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29-MAR-1996;
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Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic; Fc receptor mediated phagocytosis; immunogenic response; neuroprotective; amyloid precursor protein; Alzheimer's disease.
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Pred. No. 1.8;
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100.0%; Pred. No. 1...
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Best Local Similarity
8; Conserve
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                                                                                                                           Homo sapiens.
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Disclosure; Figure 19; 143pp; English.
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                                                                                                                                                                                                                                   disease associated with amyloid deposits of amyloid precursor protein (APP) Abeta fragments in the brain of a patient, which comprises administering to the patient: (a) an antibody that binds to abeta, the antibody binds to an amyloid deposit and induces a clearing response (For receptor mediated phagocytosis) against it (b) a polypeptide containing an N-terminal segment of at least residues 1-5 of Abeta, or (c) an agent that induces an immunogenic response against residues 1-3 to 7-11 of Abeta. The products of the invention have nootropic and neuroprotective activity. The method is also useful for monitoring a course of treatment being administered to a patient e.g. active and passive immunization. The products of prophylactic and therapeutic treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fc receptor mediated phagocytosis; immunogenic response; neuroprotective; amyloid precursor protein; Alzheimer's disease.
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                                                                                                                          Preventing or treating a disease associated with amyloid deposits, especially Alzheimer's disease, comprises administering amyloid
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                                                               Yednock T;
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                                                                                                                                                                                        Disclosure; Figure 19; 143pp; English.
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                                                              Bard F, Vasquez NJ,
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100.0%;
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Best Local Similarity
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28-MAY-1999;
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                                                               Schenk DB,
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activity. The method is also useful for monitoring a course of treatment being administered to a patient e.g. active and passive immunization. The methods are useful for prophylactic and therapeutic treatment of Alzhelmer's disease.
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This invention describes a novel method of preventing or treating a disease associated with amyloid deposits of amyloid precursor protein (APP) Abeta fragments in the brain of a patient, which comprises administering to the patient. (a) an antibody that binds to Abeta, the antibody binds to an amyloid deposit and induces a clearing response (Foreceptor mediated phagocytosis) against it (b) a polypeptide containing an N-terminal segment of at least residues 1-5 of Abeta, or (c) an agent that induces an immunogenic response against residues 1-3 to 7-11 of Abeta. The products of the invention have nootropic and neuroprotective
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22-AUG-2000; 2000US-226867P.
15-AUG-2001; 2001US-0930915.
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA;
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                                                            the C-terminal residue or in which a C-terminal Cys is replaced by another residue. The chimer particles are most stable on storage in aqueous compositions that are particles are most stable on storage in aqueous compositions that are particles of similar sequence that lack any C-terminal Cys residues. The chimer molecule exhibits the self-assembly not exhibiting the nucleic acid binding of those native particles, and excellent B cell and T cell immunogenicities. The chimer particles are typically prepared in higher yield than similar particles that are free of a C-terminal Cys. The particles are often far more immunogenic than the similar conjugates that lack a C-terminal Cys. Immunogenic than particles assembled from the chimer molecules are enhanced as compared to similar particles assembled from collmer molecules lacking at least one C-terminal Cys. AAU33802-AAU3397 represent immunogenic HBc particles and related sequences of the invention.
               develop an immune response. The immunogenic particles formed using (I) are substantially free of binding to nucleic acids, and are most stable than the particle formed from otherwise identical HBc chimer that lacks
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inoculated animal for a time period sufficient for that animal to
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2;
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99US-0153406.
99US-0159783.
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ses 8; Conservative
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15-OCT-1999;
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form

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peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB9241 represent peptides which can be used in the exemplification of the present invention.
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99US-0153406.
99US-0159783.
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Synthetic.
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15-OCT-1999;
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comprising therebentically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity of the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.
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               Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes.

AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a modified therapeutic peptide (I)
 administration due to rapid degradation by peptidases in the body
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                                                                                                                                                                                  68.4%; Score 39; DB 22; Length 14; 100.0%; Pred. No. 2.6; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           AAB91815 standard; Peptide; 14 AA.
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99US-0153406.
99US-0159783.
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10-SEP-1999;
15-OCT-1999;
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AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                              Score 39; DB 22; Length 14; Pred. No. 2.6;
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                                                                       100.0%; Preu. ...
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                                                               68.48;
                                                                                       8; Conservative
                                                                          Best Local Similarity
                                       14 AA;
                                                                                                                               3 VGSNKGAI 10
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November 9, 2002, 13:59:59; Search time 13.0769 Seconds (without alignments) 22.500 Million cell updates/sec
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Compugen Ltd.
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                                                                                                                                                                                                                                                                                         262574 seqs, 29422922 residues
GenCore version
Copyright (c) 1993 - 2002
                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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57
1 CVGSNKGAIC 10
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Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 4 Appli	· -	1	۷,	. 4	· 6	, ,	36,	36,	Sequence 40, Appl	16,		, -	Sequence 68. April	<u>,</u>	Datent NO 526232	. e		7		· ~	ì	Sequence 2. Appli	2	ì ,-	à	Sequence 3, Appli
		ID	US-09-163-095-4	-163	-30	-609	-08-475-		US-08-612-785B-16	US-08-612-785B-36	US-08-612-785B-39	-08-612-	US-08-617-267C-16	9-060-609-80-	US-08-302-808-1	US-07-737-371E-68	US-08-986-948-1	2332-1	3-304-585-	-80-	US-08-609-090-7	US-08-682-245A-1	US-08-986-948-2	US-07-744-767A-1	US-08-235-400-2	-08	-585	•	-08-302-80
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æ	Query	Match		68.4	œ	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4	68.4
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1-757-557-80-511	T *67 608 80 50	US-07-737-371E-69	US-08-682-245A-2	US-08-986-948-3	US-08-461-216-1	US-08-959-148-1	US-09-242-724-22	US-08-723-661B-1	US-09-062-365-3	PCT-US92-06700-1	US-07-819-361-1	US-08-302-808-4	US-08-682-245A-3	US-08-986-948-4	US-07-744-767A-2	US-08-179-574-1	11 11 11 11 11 11 11 11 11 11 11 11 11	US-U8-2/1-162-5	ALTGNMENTS	CTHICHES
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                                                                                   GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
TITLE OF INVENTION: METHEDS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: ALZHEIMER'S DISEASE
TITLE OF INVENTION: ALZHEIMER'S DISEASE
FILE REPERENCE: B096-09A2
CURRENT APPLICATION NUMBER: US/09/163,095
CURRENT APPLICATION NUMBER: DCT/US97/04966
EARLIER APPLICATION NUMBER: 1997-03-29
EARLIER APPLICATION NUMBER: 08/625,765
EARLIER PILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4
LENGTH: 10
                                              ; Sequence 4, Application US/09163095
; Patent No. 6242416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Cyclic peptide US-09-163-095-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Matches 10; Conserv
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RESULT 1
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1 CVGSNKGAIC 10 рp

RESULT 2

US-09-163-095-1

Sequence 1, Application US/09163095

Sequence 1, Application US/09163095

Patent No. 642416

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Yaar, Mina

TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING

TITLE OF INVENTION: ALZHEIMER'S DISEASE

FILE REFERENCE: BU96-09AZ

CURRENT APPLICATION NUMBER: US/09/163,095

CURRENT PILING DATE: 1998-09-29

EARLIER APPLICATION NUMBER: PCT/US97/04966

EARLIER FILING DATE: 1997-03-28

BARLIER PILING DATE: 1997-03-28

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US-08-475-579A-4
                                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT: Manglio, John E.

APPLICANT: Manglio, John E.

APPLICANT: Manglio, Patrick W.

TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND

TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.

STREET P.O. Box 581415

CITY: Minneapolis

STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                               Query Match 68.4%; Score 39; DB 4; Length 8; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 8; Conservative 0; Mismatches 0; Indels
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ZIP: 55488-1415
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
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EARLIER FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.(
TELECOMMUNICATION INFORMATION:
TELEFHONE: 612-305-1217
TELEFAX: 612-305-1217
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08304585 Patent No. 5721106
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-09-163-095-1
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Sequence 4, Application US/08475579A

Facent No. 5854215

GENERAL INFORMATION:
APPLICANT: Mark A. Findeis et al.
APPLICANT: Mark A. Findeis et al.
TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggre;
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTEFFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.4%; Score 39; DB 2; Length 33; 100.0%; Pred. No. 3.2; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                              COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 029-FEB-1996
CLASSIFICATION S30
ATTORNEY/AGENT INFORMATION:
NAME: KTABUS, ETIG J.
REGISTRATION NUMBER: 36,190
REGISTRATION NUMBER: 36,190
REGISTRATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM FOC Compatible
COMPUTER: TBM FOC COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN 1995
CLASSIFICATION: 514
                                                                                                                                                                                                        ADDRESSEE: LOWE PRICE LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-684-1124 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
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Best Local Similarity 100.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                    Virginia
: USA
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24 VGSNKGAI 31
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CITY: Boston
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Gaps

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Indels

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Mismatches

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8; Conservative

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Matches
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0
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APPLICANT: Maggio, John E.
APPLICANT: Mangio, John E.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIME:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mucting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. BOX 581415
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%; Score 39; DB 1; Length 35; 100.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 34; 3.3;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
GURRBUT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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               APPLICATION NUMBER: 08/404,831
FILING DATE: 14-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KATA, CATHORING: P41,106
REGISTRATION NUMBER: P41,106
REFERENCE/POCKET NUMBER: PPI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFRAX: (617)242-4214
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                        68.4%; Score 39; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08304585 Patent No. 5721106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 35 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                    peptide
internal
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PRIOR APPLICATION DATA:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     linear
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MOLECULE TYPE:
FRAGMENT TYPE:
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US-08-304-585-6
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APPLICANT: Findeis, Mark A. et al.
ATITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
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100.0%; Pred. No. 3.3;
tive 0; Mismatches
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PRIOR APPLICATION DATA:

PELLING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION DATA:

ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/08612785B Patent No. 5854204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      US-08-612-785B-16; Sequence 16, Application US/08612785B; Patent No. 5854204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DeConti, Giulio A. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)742-4214 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
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STREET: 20
TWY: Boston
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                         2 VGSNKGAI 9
2 VGSNKGAI 9
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68.4%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                       CLASSIFICATION DATA:

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

PROPLICATION DATA:

PROPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PREISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: 31,503

TELECOMMUNICATION INPORMATION:

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TELECOMMUNICATION INPORMUNICATION INPORMATION INPOR
                                                 APPLICATION NUMBER: US/08/612,785B FILING DATE: Herewith
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.(
Matches 8; Conservative
              CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 35 amino
TYPE: amino acid
TOPOLOGY: linear
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ZIP: 02109-1875
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US-08-612-785B-40
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Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FLING DATE: Herewith
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/N 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION NUMBER: US/N 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US/N 08/475,579
FILING DATE: US/N 08/40,998
FILING DATE: O7-JUN-1995
ATPONICATION NUMBER: US/N 08/548,998
FILING DATE: Z-OCT-1995
ATPONICATION NUMBER: US/N 08/548,998
FILING DATE: US/N 08/548,998
FILING DATE: US/N 08/548,998
FILING DATE: US/N 08/548,998
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: DECORT, GILLIO A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 35 amino acids
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FRAGMENT TYPE: internal
                                                                                                                                                                                                           Massachusetts
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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Gaps
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Score 39; DB 2; Length 35; Pred. No. 3.3;
                                                                                                                                                                                                                                               Sequence 40, Application US/08612785B
Patent No. 584204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Apprepation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-70N-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-70N-1995
FILING DATE: 27-0CT-1995
ATTORNEY/AGENT INFORMATION:
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us-09-632-748-4.rai

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Best Local Similarity 100.0
Matches 8; Conservative
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STATE: Virginia
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 VGSNKGAI 31
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                                                             2 VGSNKGAI 9
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                                                                                                                                                               RESULT 12
US-08-609-090-6
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100.0%; Pred. No. 3.3;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation NUMBER OF SEQUENCES: 45
CORRESSONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: CSSN 08/475,579
FILING DATE: 27-OCT-1995
ATPONENTY/AGENT INFORMATION:
NAME: APOCAT: CSIN110.
NAME: DeConti, Giulio A.

REGISTRATION NUMBER: 31,503
REFERENCE FOCKET NUMBER: 91,503
REFERENCE FOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TYPE: Jinear
MOLECULE TYPE: peptide
RAGMENT TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATJUMENT DECORT, GIULIO A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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US-08-617-267C-16
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68.4%; Score 39; DB 4; Length 35;

Query Match

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Patent No. 5840838
Sequence Information US/08609090
SENERAL INFORMATION:
APPLICANT: HENGLE, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: ARKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
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                        Indels
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APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090 FILIG DATE: 29-FEB-1996 CLASSIFICATION: 530
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100.0%; Pred. No. 3.3; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LOWE PRICE LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIF: 4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08302808
Patent No. 5750349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFRENCE/DOCKET NUMBER: 434-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-684-111.
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.4
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-6
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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US-08-986-948-1
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Sequence 68, Application US/0773731E
Fatent No. 5876548

GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET 225 Franklin Street

CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.4%; Score 39; DB 1; Length 38; 100.0%; Pred. No. 3.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                   CUMPUTER: LED. COMPUTER:
CUMPUTER: LED. COMPUTER:
CUMPRENT PAPPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFCATION ATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1993
APPLICATION NUMBER: 010132/1993
APPLICATION NUMBER: 01032/1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
APPLICATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 antho acids
                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO FRAGMENT TYPE: NO ORIGINAL SOURCE: US-08-302-808-1
                                                                                USA
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                                                           STATE: MA
COUNTRY: US
ZIP: 02019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODARA, Asano
APPLICANT: OTARA, Asano
APPLICANT: MITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN 130 WATER STREET
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                       NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFREEMCE/POCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: 019035/1993
05-FEB-1993
MBER: 286985/1993
                                                                                                                                        FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/08986948
; Patent No. 5955317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.C
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-737-371E-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 VGSNKGAI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 W
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VGSNKGAI 9
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ZIP: 02019
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PFILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORIST, 20-DE-1993
ATTORIST, 28-DEC-1993
ATTORIST, 28-DEC-1993
ATTORIST, 20-DE-1994
ATTORIST, 20-
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GenCore version 5.1.3
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9, 2002, 13:56:34; Search time 33.8462 Seconds (without alignments) 39.370 Million cell updates/sec OM protein - protein search, using sw model November Run on:

US-09-632-748-9 57 1 CATDIKGAEC 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

Louissy_Lulius

1. \$IDS2/gcgdata/geneseqyeembl/AA1980.DAT:*

2. \$IDS2/gcgdata/geneseqyeembl/AA1981.DAT:*

3. \$IDS2/gcgdata/geneseqyeembl/AA1981.DAT:*

4. \$IDS2/gcgdata/geneseqyeembl/AA1981.DAT:*

5. \$IDS2/gcgdata/geneseqyeembl/AA1981.DAT:*

5. \$IDS2/gcgdata/geneseqyeembl/AA1986.DAT:*

6. \$IDS2/gcgdata/geneseqyeembl/AA1985.DAT:*

7. \$IDS2/gcgdata/geneseqyeembl/AA1985.DAT:*

8. \$IDS2/gcgdata/geneseqyeembl/AA1980.DAT:*

8. \$IDS2/gcgdata/geneseqyeembl/AA1980.DAT:*

8. \$IDS2/gcgdata/geneseqyeembl/AA1990.DAT:*

9. \$IDS2/gcdata/geneseqyeemseqyeembl/AA1990.DAT:*

11. \$IDS2/gcdata/geneseqyeemseqyeembl/AA1991.DAT:*

12. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

13. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

14. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

15. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

16. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

17. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

18. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

20. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

21. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

22. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

23. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

24. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

25. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

26. \$IDS2/gcdata/geneseqyeembl/AA1991.DAT:*

27. \$IDS2/gcdata/geneseqyeeneseqyeembl/AA1991.DAT:*

28. \$IDS2/gcdata/geneseqyeeneseqyeembl/AA1991.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Cyclic peptide use	Human secreted pro	Propionibacterium	Novel human diagno	Drosophila melanog	Novel human diagno	Human ORFX protein	Amino acid sequenc	Drosophila melanog	Amino acid sequenc
ID	AAY39234	AAB51727	AAU49201	ABG25236	ABB60266	ABG28140	ABP04269	AAB31165	ABB67145	AAB31164
DB	20	21	22	22	22	22	23	22	22	22
Query Match Length DB ID	10	311	181	420	2703	554	56	704	166	977
Query Match	100.0	70.2	66.7	66.7	66.7	62.3	61.4	61.4	61.4	61.4
Score	57	40	38	38	38	35.5	35	35	35	35
Result No.	н	7	m	4	S	9	7	60	თ	10

99WO-US02362. 98US-0018194.

03-FEB-1999; 04-FEB-1998;

12-AUG-1999

in orphan in TEK ty io acid so io acid so in anglo in Tie2 in PRO73	NGF derived struct NGF derived struct Peptide to induce Murine nerve growt Rat nerve growth f Human nerve growth f	Conserved NGF regi Conserved NGF regi Nerve growth facto Synthetic Nerve gr (2347) NNGF. Synt (9-36) NNGF. Synt (136-62) NNGF. Synt (16-62) NNGF. Synt	Human Oktr protein Beta lactamase sig Human nerve growth Chimeric neurotrop NGF, mouse. Mus m Sequence encoded b Human nerve growth Human NGF HiddlII-	Variant human beta Nerve growth facto Human betarve g Chimeric neurotrop Chimeric neurotrop Chimeric neurotrop
AAR45440 AAR73953 AAX30318 AAG65945 ABB95463 AAB984857 AAW8844857	AAR83764 AAR83761 AAP90623 AAG64913 AAG64915 AAG64917	AAR41747 AAR41748 AAR07158 AAR07161 AAR13393 AAR13393	ABF10396 AAR15045 AAR21874 AAR29493 AAP40040 AAP90133	AAR13472 AAR77420 AAB03347 AAR21863 AAR21864 AAR21864
15 16 22 23 23 23 20 20	16 10 22 22 23	411111111111111111111111111111111111111		12 13 13 13
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	00000000000000000000000000000000000000			
35 35 35 35 35 35 55	3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	* * * * * * * * * * * * * * * * * * *	* * * * * * * * * *	**************************************
11 12 14 15 16 17 18	19 22 23 24	25 22 22 33 33 31 31 31	2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

ALIGNMENTS

Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor; NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid; Alzheimer's disease; pseudo-ligand; hair growth; hair colour; skin colour; alopecia areata; male pattern baldness. 10 /note= "C-terminus is attached via a peptide bond to the N-terminus amino acid at position 1" _note= "N-terminus is attached via a peptide bond to the C-terminus amino acid at position 10" Cyclic peptide used to inhibit p75NTR mediated apoptosis. Location/Qualifiers AAY39234 standard; peptide; 10 AA. 23-NOV-1999 (first entry) Key Modified-site Modified-site WO9939728-A2 Synthetic. AAY39234; RESULT 1 AAY39234

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This sequence is a cyclic peptide which competes with and competitively inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR). P75NTR is a low affinity nerve growth factor (NGF) receptor which is expressed by melanocytes and keratinocytes of the basal epidermis. Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2 protein. If the receptor is occupied by appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other examples of appropriate ligands include this cyclic peptide. This peptide is based on the p75NTR in Alzheimer's disease. This cyclic peptide can be used in methods involve using this peptide or peptide can be used in methods involve using this peptide or peptides call death. The methods involve using this peptide or peptides Apy39233/x39235 to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting a poptosis. The new method can induce or maintain hair growth hair colour or skin colour. Inducing or maintaining hair growth is useful for treating alopecia areata or male pattern baldness in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiproliferative, cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; nervous system disorder; Alzheimer's disease; ocular disorder; wound healing; skin aging.
                                                                                                               Controlling or manipulating melanocyte and keratinocyte cell death,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 57; DB 20; Length 10; 100.0%; Pred. No. 0.0029; 10e 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein sequence encoded by gene 3.
                                                                                                                                 useful for treating, e.g. alopecia areata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB51727 standard; Protein; 311 AA.
                                                                                                                                                                       Claim 4; Page 40; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1999; 99US-0128701.
20-JAN-2000; 2000US-0177166.
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                                    Eller M, Gilchrest BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM,
(UYBO-) UNIV BOSTON.
                                                                          WPI; 1999-539950/45.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CATDIKGAEC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Polynucleotide sequences AAC93422 - AAC93449 represent cDNA encoding human secreted proteins AAB51724 - AAB51777. Sequences AAB51786 - AAB51825 represent alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
                                                                                                                                                                                                                                                                                                                           vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; variotide; pothalmalogical; and vulnerary. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Oligonucleotide AAC93413 - AAC93421 and peptide AAB51723 are
                                         New nucleic acid molecules encoding 48 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used in the isolation and characterisation of the proteins and polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.2%; Score 40; DB 21; Length 311; 50.0%; Pred. No. 60; 2; Indels iive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #10097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; osteopathic; neuroprotectant.
                                                                                                                            Disclosure; Page 446; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU49201 standard; Protein; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-199047P.
2000US-208841P.
2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2001; 2001WO-US12865.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 5; Conserva:
WPI; 2000-619226/59
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252 CSTDVRGQHC 261
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07-JUL-2000;
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Page 3

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o;
                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. A caces is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 77;
1; Mismatches 3; Indels
                                   Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                   Wang SS,
                                 Skeiky YAW, Persing DH, Mitcham JL, Wang S.
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                       Example 1; SEQ ID No 10396; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #25227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG25236 standard; Protein; 420 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
60.0%;
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Query Match
Best Local Similarity 60.0°,
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
                                                                                                                                                                          treating acne vulgaris
                                                                                   WPI; 2001-616774/71.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CATDCRAARC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 181 AA;
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                                                                                                     N-PSDB; AAS59545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymersae chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 38; DB 22; Length 420; 50.0%; Pred. No. 1.8e+02; Live 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                         Claim 20; SEQ ID No 55595; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB60266 standard; Protein; 2703 AA.
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Best Local Similarity
تامر 5; Conserva
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               2001-639362/73.
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353 CSRDLQGTEC 362
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                              N-PSDB; AAS89423
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                                                                                                                        biodiversity
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N-PSDB; ABN20021
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                                                                                                                                                                                                                                                                                                                                                                                       ABP04269;
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                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                          (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                  Gaps
                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                    Disclosure; SEQ ID NO 7590; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                         66.7%; Score 38; DB 22; Length 2703; 60.0%; Pred. No. 1.1e+03; ive 1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 58499; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #28131.
                                                                                                                                                                                                                                                                                                                                                                                       ABG28140 standard; Protein; 554 AA.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                        437 CATGYKGVDC 446
                                                                                                                                                                                                                                   2703 AA;
                                                                                                                                                                                                                                                                    Local Similarity
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 N-PSDB; ABL04369
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                                              Interactions
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                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               ABG28140;
                                                                                                                                                                                                                                                            Query Match
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polyprucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity amin to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.3%; Score 35.5; DB 22; 70.0%; Pred. No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ORFX protein sequence SEQ ID NO:8520.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP04269 standard; Protein; 56 AA.
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29-AUG-2000; 2000US-228716P.
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leach MD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-106308/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554 AA;
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(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 to the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP001010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX associated disorder. In humans, and in the manufacture of a medicament for treating syndrome associated with ORFX associated disorder. ORFX polyucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, osteoarthritis, hearforthage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, various immune deficiencies mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, autoimmune thyroiditis, myasthenia gravis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, pone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein; receptor tyrosine kinase; Tek; Fc portion; immunoglobulin G1; IgG1; anglogenesis; tumour; ocular necvascularisation; inflammatory disease; arthritis,; rheumatism; psoriasis; eye disorder; diabetic retinopathy; necvascular glaucoma; retinoblastoma; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; graft necvascularisation; cancer; metastatic sarcoma; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                        N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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/note= "Tek extracellular domain fragment"
473..704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 23; Length 56;
Pred. No. 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a Tek/Fc fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB31165 standard; protein; 704 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.4%;
55.6%;
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Les 5; Conservative
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14 STDVHGAQC 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB31165;
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extracellular domain of the human receptor tyrosine kinase Tek and the From Fortion of human immunoglobulin (19) G1. The Tek fragment lacks all cretains the ability to bind at least one Tek ligand. The fusion polypeptide is an angiogenesis inhibitor, and a Tek antagonist. The polypeptide is an angiogenesis inhibitor, and a Tek antagonist. The polypeptide is an angiogenesis inhibitor, and a Tek antagonist. The polypeptide or solubbe Tek multimer, antibodies or antibody fragments are useful for treating a mammal having a disease or condition mediated by angiogenesis, e.g. a solid tumour a condition or disease characterized by coular neovascularisation. In particular, the Tek antagonists are useful for treating or preventing inflammatory diseases (e.g. arthritis, rheumatism or psoriasis), certain eye disorders (e.g. diabetic retinopathy of prematurity, neovascular glaucoma, retrolental fibroplasia, rubeosis, uveitis, macular degeneration or graft neovascularisation), cancer (e.g. metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                  New Tek polypeptides antagonist having a fragment of the Tek extracellular domain, useful for treating mammals with a disease mediated by angiogenesis, e.g. tumors, ocular neovascularisation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                           The present sequence represents a fusion protein comprising the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.4%; Score 35; DB 22; Length 704; 60.0%; Pred. No. 9.3e+02; .ive 1; Mismatches 3; Indels
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                                    Fanslow WC;
                                                                                                                                                                                         Claim 17; Page 37-39; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB67145 standard; Protein; 766 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 60.0
کمت 6; Conservative
                                  Borges LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                          inflammatory diseases
(IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC, Adams M,
                                                                   WPI; 2001-112149/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL11248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical
                                  Cerretti DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB67145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein; receptor tyrosine kinase; Tek; Fc portion; immunoglobulin G1; IgG1; angiogenesis; tumour; ocular neovascularisation; inflammatory disease; arthritis,; rheumatism; psoriasis; eye disorder; diabetic retinopathy; retinopathy; neovascular glaucoma; retinoblastoma; retrolental fibroplasia; rubeosis; uveitis; macular degeneration;
                                                                                          is
                                                                                                                                                                             (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed The sequence data for this patent did not format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insectiods. Therapetics in higher eukaryotes for the development of insectiodes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABL30511), expressed DNA sequences (ABLIGITG-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Tek polypeptides antagonist having a fragment of the Tek extracellular domain, useful for treating mammals with a disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neovascularisation; cancer; metastatic sarcoma; carcinoma;
                                                                                                                                                                                                                                                                                                               ;
0
                                              English.
                                                                                                                                                                                                                                                                                 22; Length 766;
                                                                                                                                                                                                                                                                                                              1; Indels
                                          ID NO 28227; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19..745
/note= "Tek extracellular domain"
746..977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a Tek/Fc fusion protein.
                                                                                                                                                                                                                                                                                  DB 22;
1e+03;
                                                                                                                                                                                                                                                                                 Score 35; DB 2
Pred, No. 1e+03
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  МС;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Fc portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB31164 standard; protein; 977 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retrolental fibroplasia; rubeosis;
graft neovascularisation; cancer; m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanslow
                                                                                                                                                                                                                                                                                  61.4%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000WO-US15706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0137889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borges LG,
                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PI; 2001-112149/12.
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            463 CLTDVQGSE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulation.
                                                                                                                                                                                                                                                     766 AA;
                                                                                                                                                                                                                                                                                                                                          1 CATDIKGAE 9
                                              Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200075323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerretti DP,
                  interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31164;
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mound
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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The present sequence represents a fusion protein comprising the extracellular domain of the human receptor tyrosine kinase Tek and the extracellular domain of the human receptor tyrosine kinase Tek and the reportion of human immunoglobulin (19) 61. The Tek fragment lacks all or part of human immunoglobulin (19) 61. The Tek fragment lacks all or part of the region containing fibronectin type III (FNIII) motifs, and retains the ability to bind at least one Tek ligand. The fusion polypeptide is an angiogenesis inhibitor, and a Tek antagonist. The polypeptide or soluble Tek multimer, antibodies or antibody fragments are useful for treating a mammal having a disease or condition mediated by angiogenesis, e.g. a solid tumour a condition or disease characterized by coular neovascularisation. In particular, the Tek antagonists are useful for treating or preventing inflammatory diseases (e.g. arthritis, rheumatism or psoriasis), certain eye disorders (e.g. diabetic retinopathy, retinopathy of prematurity, neovascular glaucoma, retinopathy of prematurity, neovascular glaucoma, retinopathy of prematularisation), cancer (e.g. metastatic egeneration or graft neovascularisation), cancer (e.g. metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
mediated by angiogenesis, e.g. tumors, ocular neovascularisation or
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 22; Length 977;
Pred. No. 1.3e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Cys of immunoglobulin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Cys of immunoglobulin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            746..772
/note= "transmembrane region"
211..340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibodies; PCR; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "claimed fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "claimed fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "EGF-like repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR45440 standard; Protein; 1124 AA.
                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human orphan receptor kinase.
                                                                                                                                                                                                                                                                                                                                                                                       61.4%;
                                                Claim 41; Page 34-37; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-US06093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0905600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 19..745
                  inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 CATGWKGLQC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 102
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CATDIKGAEC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 44
                                                                                                                                                                                                                                                                                                                                                         977 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ork; ligands;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-1994
                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR45440;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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AAR45440
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Gaps

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The present sequence represents the TEK protein, also known as TIE2 protein. TEK is a receptor tyrosine kinase. TEK contains epitopes which bind to MHC. The presentation of TEK epitopes can also stimulate the per cell and/or cytotoxic T cell responses. The immune response is directed against endothelial cells in the tumor-associated vasculature and includes production of antibodies that bind to the cells, causing coaqulation and thrombosis. The immune response is targeted to endothelial cells lining blood vessels of the tumor (these cells overexpress Tek), so damage to even a few cells will kill many tumor cells. These target cells are accessible to the immune response and problems of antigenic heterogeneity, MHC loss and resistance to apoptosis (associated with epithelial cells) are unlikely to occur in normal endothelial cells. TEK epitopes (see AAY30320-24) are used to generate antibodies, and for prevention and treatment of cancer. The peptides, and recombinant DAR constructs or viral vectors that express them, are useful as anticancer vaccines to target endothelial
                                                                                                                                                                                                                                                                                                   TEK protein; TIE2 protein; receptor tyrosine kinase; T cell response; immune response; endothelial cell; tumor-associated vasculature; coagulation; thrombosis; cancer; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides containing at least one epitope from Tek receptor tyrosine kinase, used in vaccines against cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1124;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 20; Length 11 Pred. No. 1.5e+03; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                      Amino acid sequence of TEK (also known as TIE2) protein.
   Pred. No. 1.5e+03;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durrant LG, Hewett PW, Ramage JM, Spendlove I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells that line blood vessels of the tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                       AAY30318 standard; protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 56pp; English.
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60.0%;
   60.08;
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                                                                                                                                                                                                                                     (first entry)
                    Conservative
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                                                                             289 CATGWKGLQC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 CATGWKGLQC 298
   Best Local Similarity
Matches 6; Conserv
                                                   1 CATDIKGAEC 10
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                                                                                                                                                                                                                                     15-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-1999
                                                                                                                                                                                                    AAY30318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                   RESULT 13
AAY30318
ID AAY30
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                                                                                                                                                                              Degenerate oligonucleotide primers based on the sequence conserved in the kinase domain of all receptor tyrosine kinases was used for PCR of single stranded cDNA from human placental polyA mRNA. PCR prod. HPK-6 contained a novel sequence which was used as a probe to isolate longer fragments from a human placental cDNA library. One clone contained the entire coding region and was called the ork gene. The gene prod. shown can be used as a research tool in in vitro assays for detection of ork, its ligands or their interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tie-2; receptor-tyrosine kinase; DNA primer; cancer; angiogenesis;
vasculogenesis; tek.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tie-2 receptor tyrosine kinase and related nucleic acid - and methods for detecting tie-2 modulators for treating eg cancer, associated with angiogenesis and vasculogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                               DNA and protein sequences for orphan receptor tyrosine kinase and expression vectors for prodn. of recombinant protein and antibodies specific for the protein, useful in research
                                                                                                                                                                                                                                                                                                                                                                                  61.4%; Score 35; DB 15; Length 1124; 60.0%; Pred. No. 1.5e+03; ive 1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.4%; Score 35; DB 16; Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein is the human homolog of mouse tie-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR73953 standard; Protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 49; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TEK tyrosine kinase protein.
                                                                                                                                                Claim 13; Fig 1; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-EP03767
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                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 6; Conservative
                               WPI; 1994-026132/03.
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                                                                                                                                                                                                                                                                                                                                                   1124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 CATGWKGLQC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATDIKGAEC 10
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                                                N-PSDB; AAQ55179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Ziegler SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                     Sednence
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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The invention relates to a crystalline polypeptide, comprising the catalytic domain of a receptor tyrosine kinase Tie-2 protein. The crystalline forms are useful for identifying inhibitors of a Tie-2 protein as well as determining the three dimensional structure of a the catalytic domain of a Tie-2 polypeptide. A Tie-2 inhibitor may be used to treat a Tie-2 dependent condition in a patient (especially a human), where the condition is characterized by excessive vascular proliferation e.g. a hyperproliferative disorder, cancer (e.g. sarcoma, osteona, melanoma, lupphona, and leukemia), a cardiovascular condition (myopla, chronic retinal detachment, conjunctivitis, osteona, melanoma, lupphona, chronic retinal detachment, conjunctivitis, an ocular condition (myopla, chronic retinal detachment, conjunctivitis, retinopathy, and macular degeneration), von Hippel Lindau disease, pemphigoid, psoriasis, paget's disease, polycystic kidney disease, fibrosis, sarcoidosis, cirrhosis, inflammatory bowel disease, chronic inflammation, synovitis, inflammatory bowel disease, chronic inflammation detacting and promote angiogenesis or vasculogenesis (in combination with a pro-angiogenic growth factor). The present sequence represents the human Tie-2 protein sequence.
                                                                                                                                                                                                              Tie-2; catalytic domain; receptor tyrosine kinase; crystalline; human; cytostatic; vasotropic; antianemic; antiarteriosclerotic; nephrotropic; opthalmological; hepatotropic; antithyroid; antiinflammatory; antiulcer; gastrointestinal; antirheumatic; osteopathic; antiarhritic; hemostatic; antipsoriatic; dermatological; immunosuppressive; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "catalytic domain; specifically claimed fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dixon RW, Hoeffken HW, Allen K, Bellamacina C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crystalline polypeptide useful for identifying inhibitors of a Tie-2 protein as well as determining the three dimensional structure of a polypeptide comprising the catalytic domain of a Tie-2 polypeptide -
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Pred. No. 1.5e+03;
1; Mismatches 3; Indels 0
                      AAG65945 standard; protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                 Amino acid sequence of human Tie-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 1; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.4%;
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                                                                                                                    11-FEB-2002 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                     AAG65945;
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AAG65945
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Human; anglogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                         Human angiogenesis related protein PRO734 SEQ ID NO: 82.
                 ABB95463 standard; Protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0802706.
2001US-0808689.
2001US-0816744.
2001US-0828366.
2001US-0854208.
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20000W - 0739238
2000W - 0539873
2000W - 0532678
2000W - 0747259
2000W - 0747259
2001US - 076769
2001US - 0796498
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2000WO-US23522.
2000WO-US23328.
2000US-230978P.
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2000US-0664610.
2000US-0665350.
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2001US-0866034,
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2001WO-US17800
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                                                      19-JUL-2002 (first entry)
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GURNEY A L.
HILLAN K J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENENTECH INC.
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PAN J.
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FERRARA N.
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                                                                                                                                                             WO200208284-A2.
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                                                                                                                                                                                                                                                                                   24-AUG-2000;
07-SEP-2000;
15-SEP-2000;
18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000;
10-NOV-2000;
01-DEC-2000;
                                                                                                                                           Homo sapiens.
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08-NOV-2000;
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20-DEC-2000;
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                                    ABB95463;
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(GODD/)
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RESULT 15
        ABB95463
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(PAON/) PAONI N F. (STEP/) STEPHAN J F. (WATA/) WATANABE C K. (WILL/) WILLIAMS P M.

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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, emothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                    Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                   One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 82; 567pp; English.
                                                                                                                                                                                                        WPI; 2002-171999/22.
N-PSDB; ABL95601.
                   (STEP/) STEPHAN J
(WATA/) WATANABE C
(WILL/) WILLIAMS P
(WOOD/) WOOD W I.
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Gaps

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Query Match 61.4%; Score 35; DB 23; Length 1124; Best Local Similarity 60.0%; Pred. No. 1.5e+03; Matches 6; Conservative 1; Mismatches 3; Indels C

Sequence 1124 AA;

Search completed: November 9, 2002, 14:01:18 Job time : 34.8462 secs

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9, 2002, 13:56:34; Search time 20.3077 Seconds (without alignments) 39.370 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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| SIDS2/gcgdata/geneseqg-embl/AA1982.DAT:*
| SIDS2/gcgdata/geneseqf-embl/AA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES

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		Description	Cyclic peptide	Human protein s	Human colon cancer	Arabidopsis tha	Arabidopsis tha	Arabidopsis tha	Arabidopsis tha	NS1 protein sed	Goose parvoviru	Barbary duck parvo
		ΩI	AAY39235	AAB95716	AAG73649	AAG08770	AAG43679	AAG08769	AAG43678	AAY97725	AAE22892	AAR85384
			20	22	22	21	21	21	21	22	23	16
	Query	Length	9	120	62	122	122	125	125	461	461	626
ф	Query	Match	100.0	100.0	89.2	89.2	89.2	89.2	89.2	89.3	89.2	89.2
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33 89.2 626 22 AAY97724 NSI protein sequen 33 89.2 626 23 AAR22891 MISCOVY duck parvo	3 80 2 627 22 AAVO7722 Ben protein s	3 89.2 627 22 AAY97723 Rep	3 89.2 627 23 AAE22889 Barbarie duc	3 89.2 627 23 AAE22890	3 89.2 718 22 AAU54939 Propio	2 86.5 62 22	2 86.5 80 23 ABP43203 Human ovaria	2 86.5 81 22 AAM89278 Human	2 86.5 99 22 ABB66945 Drosop	2 86.5 448 22 AAE09321	2 86.5 494 22	2 86.5 IOI2 22 ABBSY4IU 1 83 9 34 15 AABSSCO88	1 83.8 160 21 AAG14369	1 83.8 160 21	1 83.8 164 22 AAU54953	1 83.8 184 21 AAG53397	1 63.6 163 21 AAG14368 1 63 6 313 30 AAV36680	1 83.8 225 22 AAG73600	1 83.8 252 21 AAY74897	1 83.8 266 21 AAY74898 Neisseria meningi	1 83.8 267 20 AAY38692	1 83.8 267 21 AAY74896	1 83.8 286 22 AAU17516 Novel signal tran	1 83.8 327 21 AAY95907	1 83.8 388 21 AAG07845 Arabidopsis thali	1 03.0 300 ZI AMG33331 ALGUTULOPZIS 1 03.0 1 ALGUTULOPZIS 1 03.0 1 AAG53300	1 03:0 412 21 AMBJ3390 ALBANTAOPELS CHARL 1 03:0 A13 31 ABG07844	1 83 8 596 21 AAVOSOIO	1 83.8 598 21 AAY95903 Human Goodpasture	ALIGNMENTS		19235 standard; peptide; 6 AA.	99335.	1	OV-1999 (first entry)	ic peptide used to inhibit p75-NTR mediated apoptosis.	Η.	neimer's disease; pseudo-ligand; hair growth; hair colour;	n colour; alopecia areata; male pattern baldness.
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RESULT 1	.r. 1 1235 5AAY39235 standard; peptide; 6 AA.
ă	
Ş	AAY39235;
ž ti i	23-NOV-1999 (first entry)
<u>5</u> E S	Cyclic peptide used to inhibit p75-NTR mediated apoptosis.
38	Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growt
æ	NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;
3	Alzheimer's disease; pseudo-ligand; hair growth; hair colour;
3	skin colour; alopecia areata; male pattern baldness.
ă	
SC	Synthetic.
×	
H.	Key Location/Qualifiers

/note= "N-terminus is attached via a peptide bond to the C-terminus amino acid at position 6" 6 /note= "C-terminus is attached via a peptide bond to the N-terminus amino acid at position 1" Modified-site Modified-site WO9939728-A2

99WO-US02362. 98US-0018194 03-FEB-1999; 04-FEB-1998; 12-AUG-1999

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AAG73649;
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                    methods to control or manipulate keratinocyte or melanocyte cell death. The methods involve using this peptide or peptides AAY39233-Y39234 to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting apoptosis. The new method can induce or maintain hair growth, hair colour or skin colour. Inducing or maintaining hair growth is useful for treating alopecia areata or male pattern baldness in vertebrates.
                                                                                                                       This sequence is a cyclic peptide which competes with and competitively inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR). P75NTR is a low affinity nerve growth factor (NGF) receptor which is expressed by melanocytes and keratinocytes of the basal epidermis. Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2 protein. If the receptor is occupied by appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other examples of appropriate ligands include this cyclic peptide. This peptide is based on the sequence of the binding fragment of beta-amyloid, which binds to p75NTR in Alzheimer's disease. This cyclic peptide can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602
                                                                Controlling or manipulating melanocyte and keratinocyte cell death, useful for treating, e.g. alopecia areata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 37; DB 20;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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Ishii S, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:18576
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95716 standard; Protein; 120 AA.
                        Yaar M;
                                                                                                    Claim 4; Page 40; 67pp; English.
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2000JP-0118776.
2000JP-0183767.
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                      Gilchrest BA,
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 (UYBO-) UNIV BOSTON.
                                           WPI; 1999-539950/45.
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AAB95716
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The present invention describes primer sets for synthesising 5602

(111-length cDNAs defined in the specification. Where a primer set

(211-length cDNAs defined in the specification. Where a primer set

(211-length cDNAs defined in the specifide complementary

(212 comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of

(213 complementary strand of a polynucleotide which comprises one of

(214 complementary strand of a polynucleotides; or (b) a combination

(215 complementary strand of a polynucleotide which comprises a 5'-end

(216 sequence and an oligonucleotide comprising a sequence complementary to the

(217 complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a

(218 polynucleotide comprises a 1 east 15 nucleotides and the combination of

(219 collique which comprises a 1 east 15 nucleotides and the combination of

(219 collidonicleotide comprises a 1 east 15 nucleotides and the combination of

(219 collidonicleotide comprises a 1 east 15 nucleotides and the combination of

(219 collidonicleotide comprises a 1 east 15 nucleotides and the combination of

(219 collidonicleotide comprises a 1 east 15 nucleotides and the combination of

(219 collidonicleotide comprises a 1 east 15 nucleotides and the combination of

(219 collidonicleotide comprises a 1 east 15 nucleotides)

(219 collidonicleotide comprises a 1 east 15 nucleotides)

(220 complementary the primers are useful for synthesising polynucleotides)

(221 collidonicleotide comprises allow obtaining of the full-length

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(221 collidonicleotide collides)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                              Claim 8; SEQ ID 18576; 2537pp + CD ROM; English.
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Cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P carperssion. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell of treatment of colorectal carcinomas and cancers. Administration, diagnosis and treatment of colorectal carcinomas and cancers. Administration of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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83.3%; Pred. No. 68;
7ative 0; Mismatches 1; Indels
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               Claim 11; Page 6235-6236; 9803pp; English.
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990S-0125788.
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                   Sequence 62 AA;
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99US-0139763.
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99US-0138847.
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990S-0132486.
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99US-0137222
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                                                                                                                                                                      89.2%; Score 33; DB 21; Length 122; 83.3%; Pred. No. 1.2e+02; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 54622.
                                                                                                                                                                                                                                                                            AAG43679 standard; Protein; 122 AA.
990S-0160769.
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AAY97725 standard; Protein; 461 AA. RESULT

AAY97725;

19-JUN-2001 (first entry)

NS1 protein sequence.

Fusion nucleic acid library; Rep protein; tumour cell; apoptosis; nucleic acid modification enzyme; cell death; decreased cell growth; protein-protein interaction detection; cell division; cancer therapy; protein drug discovery; pharmacogenetics; NSI protein.

Goose parvovirus.

WO200114539-A2.

01-MAR-2001

18-AUG-2000; 2000WO-US22906.

20-AUG-1999; 99US-0150004. 02-JUN-2000; 2000US-0209130.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE

Li M;

WPI; 2001-218443/22. N-PSDB; AAA91315.

New library of fusion nucleic acids each encoding a Rep protein recognized by a nucleic acid modification enzyme and a candidate protein, useful for detecting protein-protein interactions, protein drug discovery or pharmacogenetics

Disclosure; Fig 31; 106pp; English.

This sequence is the goose parvovirus NSI protein.

The invention relates to a library of fusion nucleic acids, each encoding a Rep protein, a candidate protein is a nucleic acid modification sequence or a label. The Rep protein is a nucleic acid modification enzyme. The random or directed libraries (including the cDNA libraries) can be introduced into any tumnour cell, and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The methods and compositions may also be used to detect protein protein interactions, protein drug discovery, particularly for protein drugs that interact with targets on cell surfaces, to discover DNA or nucleic acid binding proteins, using nucleic acids as targets, to screen for nucleic acid modification enzymes in expression vectors and in pharmacogenetic studies. The method for use in expression vectors and in pharmacogenetic studies. The methods can be combined with observations in the interval in the methods can be combined with observations and in killing tumour cells. The methods can be combined with observations and in killing tumour cells. be combined with other cancer therapeutics (drugs or radiation) to sensitize cells and thus induce rapid and specific apoptosis, cell death, loss of cell division or decreased cell growth after exposure to a secondary agent. NOT COULD COURT OF CO

461 AA; Sednence

°; Gaps ö 89.2%; Score 33; DB 22; Length 461; 66.7%; Pred. No. 3.6e+02; live 2; Mismatches 0; Indels Query Match
Best Local Similarity 66.7%

241 CKGSVC 246 1 CKGAIC 6 g ŏ

RESULT 9

AAE2289:

AAE22892 standard; Protein; 461 AA.

AAE22892;

09-AUG-2002 (first entry)

Goose parvovirus NS1 protein.

Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS enzyme attachment sequence; cancer therapy; protein-protein interaction; drug discovery; NSI protein; gene therapy; cytostatic.

Goose parvovirus.

. Misc-difference 68

/note= "Encoded by ATT"

WO200222826-A2

21-MAR-2002.

14-SEP-2001; 2001WO-US28702.

14-SEP-2000; 2000US-232960P.

(XENC-) XENCOR INC

Liu H; Li M, Melander C,

WPI; 2002-393969/42.

N-PSDB; AAD36286

Library of nucleic acid/protein conjugates, has a fusion of nucleic acid modification enzyme and candidate compound, and expression vector having a fusion of nucleic acids encoding NAM enzyme and the compound

Disclosure; Fig 31; 96pp; English.

protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic acid modification (NAM) enzyme (E) and candidate compound), an expression vector (with a fusion of nucleic acids encoding the enzyme and candidate protein respectively), an enzyme attachment sequence (EAS; RNA sequence), where the candidate compound and candidate protein are different and EAS and the enzyme are covalently linked. The NAP conjugates are useful in screens to assay binding to target molecules and/or to screen candidate agents for the ability to modulate the activity of the target molecule. They are useful in cancer therapy. Sequences of the invention are also useful to detect protein-protein interaction, in drug discovery, to discover pan or nucleic acid binding proteins, using nucleic acids as the targets and to screen for NAM enzymes with decreased toxicity for host cells (specifically Rep proteins with reduced toxicity). NAP conjugates are also useful in pharmacogenomic studies, for screening bioactive agents on surface cells, viruses and microbial organisms. They are also useful for screening protein expression, or proteins that a so verproduction or inhibition of protein expression, or proteins that invention are also used in gene therapy. The present sequence is invention are also used in gene therapy. The present sequence is The present invention relates to genetic libraries of nucleic acid/

461 AA; Seguence

Length 461; Score 33; DB 23; Pred. No. 3.6e+02; 89.2%; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of the non-structural protein encoded by the open reading frame (ORF) 1 contained in a fragment from the Barbary duck parvovirus strain FM. The fragment contains 3 ORFs, with ORF3 being internal to ORF2, encoding a non-structural, the VP1 and VP2 proteins respectively. The virus was isolated from a 13 day old duck that had died of Barbary duck parvovirus infection, by incubating liver extracts injected into embryonated duck eggs. The DNA was isolated from the resulting 20-25 nm viral particles. The DNA sequences encoding the non-structural, vectors, host cells or attenuated parvoviruses for use as vaccines to protect Barbary ducks and geese.
                                                                                                                                                               VP1; VP2;
                                                                                                                                              Barbary duck parvovirus fragment ORF1 encodoed non-structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequence from Barbary duck parvovirus – related vectors, transformed cells, proteins etc., useful diagnostically and
 Gaps
                                                                                                                                                                          geese.
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                                                                                                                                                               Barbary duck; parvovirus; open reading frame; non-structural; liver extract; virus particle; vector; host cell; attenuated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 16; Length 626;
Pred. No. 4.7e+02;
2; Mismatches 0; Indels
 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
Mismatches
                                                                                                                                                                                                                                 /note= "encoded by GTA"
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY97724 standard; Protein; 626 AA.
                                                                                    AAR85384 standard; Protein; 626 AA.
5;
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                                                                                                                                                                                                                                                                                                                                                   Nagy J,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 3; 39pp; French.
                                                                                                                                                                                                                                                                                          95FR-0002515
                                                                                                                                                                                                                                                                                                           94HU-0000634
                                                                                                                           09-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
4; Conservative
                                                                                                                                                                                             Barbary duck parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                            vectors, transformed ce
in protective vaccines
                                                                                                                                                                                                                                                                                                                                                 Erdei J, Kisari J,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-346564/45.
N-PSDB; AAT01190.
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                                                                                                                                                                                                                        Misc-difference
                                    241 CKGSVC 246
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                  CKGAIC 6
                                                                                                                                                                                                                                                                                                              03-MAR-1994;
                                                                                                                                                                                                                                                                                          03-MAR-1995;
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                                                                                                                                                                                                                                                                       06-0CT-1995
                                                                                                       AAR85384;
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AAY97724
ID AAY97;
Matches
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                                                                  RESULT 10
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This sequence is the muscovy duck parvovirus NSI protein.

The invention relates to a library of fusion nucleic acids, each encoding a Rep protein, a candidate protein is a protein. a targeting acquence or a label. The Rep protein is a nucleic acid modification enzyme. The random or directed libraries (including the cDNA libraries)

Can be introduced into any tumnour cell, and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The methods and compositions may also be used to detect protein protein interactions, protein drug discovery, particularly for protein drugs that interact with targets on cell surfaces, to discover DNA or nucleic acid binding proteins, using nucleic acids as targets, to screen for nucleic acid modification enzymes uncleic acids as targets, to screen for nucleic acid modification enzymes nucleic acids as targets, to screen for nucleic acid modification enzymes unth decreased toxicity for the host cells, to identify or generate Rep proteins with decreased toxicity, improved enzyme attachment sequences for use in expression vectors and in pharmacogenetic studies. The method is useful in cancer therapy and in killing tumour cells. The methods can be combined with other cancer therapeutics (drugs or radiation) to sensitize cells and thus induce rapid and specific apoptosis, cell death, loss of cell division or decreased cell growth after exposure to a
                                                                                                                                                                    Fusion nucleic acid library; Rep protein; tumour cell; apoptosis; nucleic acid modification enzyme; cell death; decreased cell growth; protein-protein interaction detection; cell division; cancer therapy; protein drug discovery; pharmacogenetics; NSI protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New library of fusion nucleic acids each encoding a Rep protein recognized by a nucleic acid modification enzyme and a candidate protein, useful for detecting protein-protein interactions, protein drug discovery or pharmacogenetics
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Pred. No. 4.7e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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02-JUN-2000; 2000US-0209130.
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19-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   Muscovy duck parvovirus.
                                                                                           NS1 protein sequence.
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to genetic libraries of nucleic acid/
protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic
acid modification (NAM) enzyme (E) and candidate compound), an expression
vector (with a fusion of nucleic acids encoding the enzyme and candidate
protein respectively), an enzyme attachment sequence (EAS; RNA sequence),
where the candidate compound and candidate protein are different and EAS
and the enzyme are covalently linked. The NAP conjugates are useful in
screens to assay binding to target molecules and/or to screen candidate
agents for the ability to modulate the activity of the target molecule.
They are useful in cancer therapy. Sequences of the invention are also
useful to detect protein-protein interaction, in drug discovery, to
seful to detect protein-protein interaction, in drug discovery, to
useful to screen for NAM enzymes with decreased toxicity for
host cells (specifically Rep proteins with reduced toxicity). NAP
conjugates and to screen for NAM enzymes with neduced toxicity in are also useful for screening proteins causing phenotypic changes such
as overproduction or inhibition of protein expression, or proteins that
also useful infectivity, etc. of the virus. Sequences of the
invention are also used in gene therapy. The present sequence is
muscoyy duck parvovirus NSI protein used in the invention.
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                                                                                                         Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS; enzyme attachment sequence; cancer therapy; protein-protein interaction; drug discovery; NS1 protein; gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library of nucleic acid/protein conjugates, has a fusion of nucleic acid modification enzyme and candidate compound, and expression vector having a fusion of nucleic acids encoding NAM enzyme and the compound
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Pred. No. 4.7e+02;
2; Mismatches 0; Indels
                                                                          Muscovy duck parvovirus NS1 protein.
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                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Liu H;
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                                                                                                                                                                                          Muscovy duck parvovirus.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            (XENC-) XENCOR INC.
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                                         09-AUG-2002
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     AAE22891;
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δ αq

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This sequence is the barbarie duck parvovirus Rep protein.

The invention relates to a library of fusion nucleic acids, each encoding a Rep protein, a candidate protein is a nucleic acid modification as sequence or a label. The Rep protein is a nucleic acid modification or enzyme. The random or directed libraries (including the CDNA libraries) can be introduced into any tumour cell, and peptides identified which by themselves induce apoptosis, cell dath, loss of cell division or decreased cell growth. The methods and compositions may also be used to detect protein-protein interactions, protein drug discovery, or particularly for protein drugs that interact with targets on cell particularly for protein drugs that interact with targets on cell concleic acids as targets, to screen for nucleic acid modification enzymes nucleic acids as targets, to screen for nucleic acid modification enzymes proteins with decreased toxicity for the host cells, to identify or generate Rep proteins with decreased toxicity, improved enzyme attachment sequences for use in expression vectors and in pharmacogenetic studies. The method is useful in cancer therapy and in killing tumour cells. The methods can be combined with other cancer therapeutics (drugs or radiation) to sensitize cells and thus induce repaid and specific apoptosis, cell death, considered to a considered cell growth after exposure to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                        Fusion nucleic acid library; Rep protein; tumour cell; apoptosis; nucleic acid modification enzyme; cell death; decreased cell growth; protein protein interaction detection; cell division; cancer therapy; pharmacogenetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New library of fusion nucleic acids each encoding a Rep protein recognized by a nucleic acid modification enzyme and a candidate protein, useful for detecting protein-protein interactions, protein drug discovery or pharmacogenetics
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66.7%; Pred. No. 4.7e+02;
Live 2; Mismatches 0; Indels
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19-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         Barbarie duck parvovirus.
                                                                              Rep protein sequence.
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Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS; enzyme attachment sequence; cancer therapy; protein-protein interaction; drug discovery; Rep protein; gene therapy; cytostatic.

Barbarie duck parvovirus Rep protein.

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This sequence is the goose parvovirus Rep protein.

The invention relates to a library of fusion nucleic acids, each encoding the invention relates to a library of fusion nucleic acids. each encoding the protein, a candidate protein, a presentation structure, a targeting sequence or a label. The Rep protein is a nucleic acid modification in the random or directed libraries (including the CDNA libraries) and publication introduced into any tumour cell, and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The methods and compositions may also be used to detect protein protein interactions, protein drug discovery, particularly for protein drugs that interact with targets on cell surfaces, to discover DNA or nucleic acid binding proteins, using surfaces, to discover DNA or nucleic acid binding proteins, using vith decreased toxicity for the host cells, to identify or generate Rep proteins with decreased toxicity, improved enzyme attachment sequences for use in expression vectors and in pharmacogenetic studies. The method is useful in cancer therapy and in killing tumour cells. The methods can be combined with other cancer therappus conditions or radiation) to sensitize cells and thus induce rapid and specific apoptosis, cell death, senondary and in virial provent after exposure to a sensitize cells and thus induce rapid and specific apoptosis, cell death, senondary and an expression or decreased cell growth after exposure to a
                                                                 Fusion nucleic acid library; Rep protein; tumour cell; apoptosis; nucleic acid modification enzyme; cell death; decreased cell growth; protein protein interaction detection; cell division; cancer therapy; protein drug discovery; pharmacogenetics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New library of fusion nucleic acids each encoding a Rep protein recognized by a nucleic acid modification enzyme and a candidate protein, useful for detecting protein-protein interactions, protein drug discovery or pharmacogenetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 27; 106pp; English.
                                                                                                                                                                                                                                                                                                            18-AUG-2000; 2000WO-US22906.
                                                                                                                                                                                                                                                                                                                                                                             02-JUN-2000; 2000US-0209130.
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                         Rep protein sequence.
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N-PSDB; AAA91313.
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protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic acid modification (NAM) enzyme (E) and candidate compound), an expression vector (with a fusion of nucleic acids encoding the enzyme and candidate protein respectively), an enzyme attachment sequence (EAS; RNA sequence), where the candidate compound and candidate protein are different and EAS and the enzyme are covalently linked. The NAP conjugates are useful in screens to assay binding to target molecules and/or to screen candidate agents for the ability to modulate the activity of the target molecule. They are useful in cancer therapy. Sequences of the invention are also useful to detect protein-protein interaction, in drug discovery, to discover DNA or nucleic acid binding proteins, using nucleic acids as the targets and to screen for NAM enzymes with decreased toxicity for host cells (specifically Rep proteins with reduced toxicity for conjugates are also useful in pharmacogenomic studies, for screening bloactive agents on surface cells, viruses and microbial organisms. They are lasto useful for screening proteins causing phenotypic changes such as overproduction or inhibition of protein capterins causing phenotypic changes such as overproduction are also used in gene therapy. The present sequence is invention are also used in gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library of nucleic acid/protein conjugates, has a fusion of nucleic acid modification enzyme and candidate compound, and expression vector having a fusion of nucleic acids encoding NAM enzyme and the compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%; Score 33; DB 23; Length 627; 66.7%; Pred. No. 4.7e+02; 11ve 2; Mismatches 0; Indels
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                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 25; 96pp; English.
                                                                                                                                                                                                                                                                                                         14-SEP-2001; 2001WO-US28702.
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                                                                                                             Barbarie duck parvovirus.
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AAE22889 standard; Protein; 627 AA.

RESULT 15 AAE22889

ò g 09-AUG-2002 (first entry)

AAE22889;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 9, 2002, 13:59:04; Search time 26.5385 Seconds (without alignments) 77.641 Million cell updates/sec Run on:

US-09-632-748-4 57 1 CVGSNKGAIC 10 Perfect score: Seguence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters; 671580 seqs, 206047115 residues Searched:

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:*

1: Sp_archea:*
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3: Sp_tungi:*
4: sp_tuman:*
5: sp_turertebrate:*
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sp_vertebrate:*
sp_unclassified:*
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SUMMARIES

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RESULT 2 Q9PD24

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RA ALVAINED L.M.C., ARIVAG D. Baia G.S., Baptista C.S.,
RA ALVAINED L.M.C., ARIVAG J.E., Bordin S., Boye J.M., Brinces M.R.S.,
RA BARTOS M.H., Bondaccorsi E.D., Bordin S., Boye J.M., Brinces M.R.S.,
RA COLONDO C., COSTA F.F., COSTA M.C.R., COSTA-NETO C.M.
RA COUTHIND L.L., CISTOFANI M., DISS NEOD E., DOCEMA C., El-DORTY H.,
RA FRAGA J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA FRAGA J.S., Franca S.C., From M. M., Frohme M., Furlan L.R.,
RA FRAGE J.S., Franca S.C., From M. M., Frohme M., Furlan L.R.,
RA FRAGE J.S., Franca S.C., From M. M. F., Gonber A.,
RA Krieger J.E., Hoheisel J.D., Junqueira M.L., Kemport E.L., Kitajima J.P.,
RA Krieger J.E., Maranca S.A., Lopes C.R., Nathado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Machado M.A., Madeira B.C., Miyaki C.Y., Monteiro VILCE.S.,
RA Manni A. Jr., Nobrega F.G., Miyaki C.Y., Monteiro VILE.S.,
RA Monni A. Jr., Nobrega F.G., Nures L.R., Coliveira M.A., Pesquero J.B.,
RA Gollyevira M.C., de Ollveira R.C., Palmieri D.A., Paris A.,
RA Gollyevira M.C., de Ollveira R.C., Palmieri D.A., Paris A.,
RA Ga Silva A.M., Madianis J.Y., Seaquero J.B.,
RA de Souza A.J., Terenzi M.F., Truelfi D., Teal S.N., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truelfi D., Teal S.N., Tsuhako M.H.,
RA Goods A.P., Terenzi M.F., Truelfi D., Teal S.N., Tsuhako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Seubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
R. Nature 406:151-15972000.
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Homo saptens (Human).
Bukaryota: Metazoa; Chordata; Craniata: Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                           Created)
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284 AA
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Interpro: IPR004107; Phage_integr_N.
Pfam; PF00589; Phage_integrase; 1.
Pfam; PF02899; Phage_integr_N; 1.
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PRT;
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EMBL; AE003985; AAF84364.1; -.
HSSP; P03700; 1AE9.
                          01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                         Phage-related protein.
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MEDLINE-93024877; PubMed-1406936; Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D., Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.; Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.; biological fluids."isolation of soluble Alzheimer's beta-peptide from biological fluids."isolation of History Nature 359:325-327(1992).
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MEDLINE-20063685; PubMed-10594237;
Konfortov B.A., Licence V.E., Miller J.R.;
"Resequencing of DNA from a diverse panel of cattle reveals a high level of polymorphism in both intron and exon.";
Manm. Genome 10:1142-1145(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                                                                                                                                                                                                                                                                            68.4%; Score 39; DB 4; Length 33; 100.0%; Pred. No. 1.2; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       InterPro: IPRO/1255, Beta-APP.
Pfam; PF03494; Beta-APP; 1.
SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;
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01-JNN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR001255; Beta-APP.
Pfam, PF03494; Beta-APP; 1.
NOV_TER
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Matches 8; Conservative
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Matches 8; Conservative
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                                        Pfam; PF03494; Beta-APP; 1.
                                                                                                     Query Match
Best Local Similarity 100.(
Matches 8, Conservative
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Matches 8; Conservative
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MEDLINE-21105969; PubMed-11158371;
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
Falazilber M.;

Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
Mol. Biol. Evol. 18:120-131(2001).

EMBL: AF215053; AAG60481.1;
InterPro: IPR004214; Conotoxin.

Pfam; PF02950; Conotoxin;
SEQUENCE 80 AA; 8724 MW; 3A516A7280D9872D CRC64;
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MEDLINE-93236601; PubMed-8476439;
Denman R.B., Rosenzcwaig R., Miller D.L.;
"A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Conus arenatus (Sand-dusted cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidae; Conidae; Conus.
                                                                                                                                                   68.4%; Score 39; DB 11; Length 79; 100.0%; Pred. No. 2.9; Live 0; Mismatches 0; Indels
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                      SEQUENCE FROM N.A.
Sambamurti K., Pinnix I., Gandhi S.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030413; AB886608.1; -.
HSSP; PO5067; 1BA4.
InterPro; IPR001255; Beta-APP.
                                                                                                                              79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;
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016014;
01-00V-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Homo sapiens (Human).
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60.08;
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Matches 6; Conserva
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NCBI_TaxID=10029;
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=93236601; PubMed=8476439;
Denman R.B., Rosenzcwaig R., Miller D.L.;
The processing of the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";
Biochem. Biophys. Res. Commun. 192:96-103(1993).
EMBL; S61380; AAB26264.2; ---
HSSP; P05067; IBA4.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                       68.4%; Score 39; DB 4; Length 82; 100.0%; Pred. No. 3; 0; Indels tive 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2002 (TrEMBLrel. 21, Last annotation update)
Beta-amyloid peptide (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Biochem. Biophys. Res. Commun. 192:96-103(1993). . . Bhali. S60721, AAB56263.2; -. HSSP, P05067; 1BA4. InterPro; IPR001255; Beta-APP.
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mutations on the processing of the beta-amyloid peptide precursor.";
Blochem. Blophys. Res. Commun. 192:96-103(1993).
EMBL; S61381; AAB26265.2; -.
HSSP; S05067; 1BA4.
InterPro; IPR001255; Beta-APP.
Pfam; PF03494; Beta-APP; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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MEDLINE-89392030; Pubmed-2675837;
Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
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                                                                                                                                                                                                                           82 AA; 8882 MW; F534AA5AE5D9230A CRC64;
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Pfam; PF03494; Beta-APP; 1.
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Best Local Similarity 100.،
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Best Local Similarity 100.
Matches 8; Conservative
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Goldgaber D., Lerman M.I., McBride O.W., Safflotti U., Gajdusek D.C., "Characterization and Chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease."; Science 235:877-880(1987).
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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuncoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AYG60733, AAL28281.1; --
FlyBase; FBGN0034396; CG15097.
InterPro; IPR000210; BTB_POZ.
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 5; Length 513;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                           68.4%; Score 39; DB 4; Length 97; 100.0%; Pred. No. 3.6; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 6.
PROSITE; PS50997; BTB; 1.
SEQUENCE 513 AA; 57551 MW; 2089D4F732514834 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              97 AA; 10884 MW; E528CDB448DE474E CRC64;
                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Amyloid protein (AD-AP) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
   97 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 AA.
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   PRT;
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=87120328; PubMed=3810169;
                                                                                                                                                                                                                                                                             EMBL; M15533; AAA35540.1; -. HSSP; P05067; 1BA4.
InterPro; IPR001888; A4_APP.
InterPro; IPR001255; Beta-APP.
Pfam; PF03494; Beta-APP; I.
PRINTS; PR00203; AMYLOIDA4.
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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   PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BERKELEY;
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SEQUENCE
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013778
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Q95SK6
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InterPro; IPR001255; Beta-APP.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 21, Last annotation update)
Amyloid protein (Fragment).
Gallius gallius (Chicken).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APP.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
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"What the evolution of the amyloid protein precursor supergene family tells us about its function.";
Neurochem. Int. 0:0-0(2000).
BEMBL: APV30341; AAPI2698.1; -.
HSSP; PO5067; IBA4.
InterPro; IPR001868; A4_APP.
         Gaps
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MEDLINE-98337885; PubMed-9671674;

Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,

Milligan C.E.;

"Increased production of amyloid precursor protein provides a substrate for caspase-3 in dying motoneurons.";

"Increased production of amyloid precursor protein provides a substrate for caspase-3 in dying motoneurons.";

"Increased production of amyloid precursor protein provides a substrate for caspase-3 in dying motoneurons.";

"Increased production of amyloid motoneurons.";

"Increased production of amyloid actoneurons.";

"Increased production of amyloid actoneuro
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   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1
SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                             534 AA.
2; Mismatches
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Matches 8; Conservative
5; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                     410 CIGGNDGTMC 419
                                                          1 CVGSNKGAIC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 VGSNKGAI 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus.
NCBI_TaxID=9031;
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                                                                                                                                                                                                            RESULT 13
093296
Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                             Query Match 68.4%; Score 39; DB 13; Length 569; Best Local Similarity 100.0%; Pred. No. 22; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC005490; AAH05490.1; -.
HSSP; P05067; 1AAP.
                                                                                                                                                                  SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;
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InterPro; IPR001868; A4_APP.
InterPro; IPR001223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF00177; A4_EXTRA; 1.
Pfam; PF001014; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00023; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00319; A4_INTRA; 1.
PROSITE; PS00380; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00280; BPTI_KUNITZ_2; 1.
Hypothetical protein; Serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 68.4 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         607 AA
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Pfam; PF02177; A4_EXTRA; I.
Pfam; PF03494; Beta-APP; I.
Pfam; PR00203; AMTLOIDA4.
SMART; SM00006; A4_EXTRA; I.
PROSITE; PS00319; A4_EXTRA; I.
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Best Local Similarity 100...
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 495 VGSNKGAI 502
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us-09-632-748-4.rsp

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 9, 2002, 13:57:44; Search time 7.69231 Seconds (without alignments) 53.919 Million cell updates/sec Run on:

US-09-632-748-4 57 1 CVGSNKGAIC 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| RIES | | Description | s sns 8 | Q29149 ursus | 028280 | 02874 | 028757 | Q28053 bos | Q95241 saimi | P05067 homo | P12023 mus n | P08592 | 029999 | 026742 | 060259 | Q25464 mytil | . 09zjc5 | P56108 | . 051160 | E P40421 | P30322 | Q9p0k1 | Q9p7m8 schiz | | P28340 | P58928 conus | P27144 homc | O3mr9 | 0snw60 | ST P41318 | 058576 | Q15173 hc | .028647 o se | |
|-----------|--------|--------------|---------|--------------|----------|----------|----------|------------|--------------|-------------|--------------|--------|------------|------------|------------|--------------|-----------|-----------|-----------|------------|------------|------------|--------------|------------|------------|--------------|-------------|------------|----------|------------|------------|------------|--------------|------------|
| SUMMARIES | } | ID | A4_PIG | A4_URSMA | A4 CANFA | A4_RABIT | A4_SHEEP | A4_BOVIN | A4_SAISC | A4_HUMAN | A4_MOUSE | A4_RAT | ADEC_ARCFU | PUR1_METTH | KLK8_HUMAN | FP2_MYTGA | TAL_HELPJ | TAL_HELPY | SYH_BORBU | RDGC_DROME | DPOM_AGABT | AD22_HUMAN | N184_SCHPO | DPOD_BOVIN | DPOD_HUMAN | CXEX_CONCN | KAD4_HUMAN | KAD4_MOUSE | KAD4_RAT | YNA6_YEAST | PSMR_METJA | 2A5B_HUMAN | 2A5B_RABIT | TRFE BOVIN |
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| | • | Match Length | 57 | 57 | 58 | 28 | 58 | 59 | 751 | 770 | 770 | 770 | 556 | 474 | 260 | 473 | 316 | 316 | 457 | 199 | 797 | 906 | 1564 | 1106 | 1107 | 30 | 223 | 223 | 223 | 303 | 430 | 497 | 500 | 704 |
| • | Query | Match | 68.4 | 68.4 | 68.4 | 68.4 | 68.4 | 68.4 | 68.4 | 68.4 | 68.4 | 68.4 | 64.9 | 63.2 | | 61.4 | 59.6 | 59.6 | | | | | | | | | | | | | | | 57.9 | |
| | | Score | 39 | | | | | | 39 | | 39 | 39 | 37 | 36 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | Э. | 33.5 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 |
| | Result | No. | п | 7 | 3 | 4 | 2 | ø | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 33 |

| Q61324 mus musculu
P27540 homo sapien | 002748 oryctolagus
P53762 mus musculu | P41739 rattus norv
Q9p193 chlamydia m | 084834 chlamydia t
001260 impatiens n | Q09853 schizosacch
Q9zdt9 rickettsia | Q9r1q8 mus musculu
P37805 rattus norv | |
|------------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|-----------------------------------------|------------------------------------------|--|
| ARNZ_MOUSE
ARNT_HUMAN | ARNT_RABIT
ARNT_MOUSE | ARNT_RAT
RIR1_CHLMU | RIR1_CHLTR | YAED_SCHPO | NP25_MOUSE
NP25_RAT | |
| 7 | | | | | | |
| 712 | 790
791 | 800
1047 | 1047 | 1616 | 199 | |
| 57.9 | 57.9 | 57.9 | 57.9 | 57.9 | 56.1 | |
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ALIGNMENTS

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strictions on it | it is in no way | commer | /annon | : | | | | | | | | | | | | | Gaps |
| | eta-a | | stomi | | | | , | e S.P | speci | | _ | PROT | | | 1 1 1 1 | a col | BL ou | is | for | ib.ch | | | | | | | | | E). | | | | | 0; |
| | [Contains: Beta-amyloid | | | dae; Sus. | | | | by M.O., Norris F.H., Pascual R., Little S.P | "Conservation of the Sequence of the Atthermet's disease whytore peptide in dog, polar bear and five other mammals by cross-species | | n Res. Moi. Brain Res. 10:299-303(1991).
princhion, princhional NEURONAL RECEPTOR WHICH COUPLES TO | INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN | | ein. | SIMILARITY: BELONGS TO THE APP FAMILY. | This SWISS-PROT entry is copyright. It is produced through a collaboration | and the | as its content | Usage by and | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | | | | | | | BETA-AMYLOID PROTEIN (POTENTIAL) | TENTTUD). | | CRC64; | Length 57; | 0; Indels |
| 57 AA. | (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
disease amyloid A4 protein homolog | nt). | Chordata; Craniata; Vertebrata; | Cetartiodactyla; Suina; Suidae; | | | | F.H., Pascu | other mamma | ,1001, | D(1991)
PEDEOR WHIC | THROUGH THE | G(O) (BY SIMILARITY). | brane prote | AFF FAMILI. | It is produ | Swiss Institute of Bioinformatics Bioinformatics and Appendix Institute. | long as | emoved. Us | t (See http
ch) | C | | | | | | Transmembrane. | | YLOID PROT | LAK | ΑГ. | 84209D88EBA82DFA | 9; DB 1; | . 0.8;
ches |
| PRT; | Created) Last sequence update) Last annotation update) yloid A4 protein homolo | (A-beta)] (Fragment). | a; Crania | odactyla; | | | 56157; | , Norris | and five | nalysis." | 10:299-30 | PATHWAY | i | ype I mem | THE APP F | pyright. | e of Bioi
Institut | non-profit institutions as long | is not r | agreemen | TOURS GETS STD: CIII) | | | PP. | | PARTIAL. | ne: | | BETA-AM | EATRACE | POTENTIAL | | Score 39; | P1
0; |
| STANDARD; | 35, Created)
35, Last sec
40, Last and
se amyloid A4 | | | | | | PubMed=16 | aney M.O. | le sequent
Lar bear | saction a | AID KES. | SIGNALING | ARITY). | CATION: T | SIMILARITY: BELONGS TO THE | try is co | Institut
formatics | t instit | statement | a license | ייייייי ר | CAA39592.1; | . A4 ADD | 5; Beta-APP | PF03494; Beta-APP; 1. | PS00319; A4_EXTRA; | Amvloid: Neurone: | - | 48 | יים ני | 57 | 6172 MW; | 68.48; | 100.0%;
vative |
| STAN | | ta-APP) | (Pig).
Metazoa; | Eutheria;
>=9823; | | OM N.A. | 17079; 1 | 3.M., Cha | dog, pol | chain re | MOI. Bra | SLLULAR S | 3Y SIMIL | CULAR LOC | KITY: BE | -PROT en | | on-profit | nd this | equires a | ellair to r | 27; CAA39 | DPOOLER4 | IPR00125 | 194; Bet | 500319; | in: Amvl | 1 | φ, | 7.7 | 5.4 | 57 AA; | | Similarity 100
8; Conservative |
| CT 1
IG
A4_PIG | 029023;
01-NOV-1997
01-NOV-1997
16-OCT-2001
Alzheimer's | protein (Beta-APP)
APP. | scrofa
ryota; | Mammalia; Euther
NCBI TaxID=9823; | [1] | SEQUENCE FROM N.A. | MEDLINE=92017079; PubMed=1656157; | Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., | "Conservat:
peptide in | polymerase chain reaction analysis."; | Brain Res. Mol. Brain Res. 10:299-303(1991). | | | | -i-SIMITTA | This SWISS | between the | use by no | modified and this statement is not removed. | entities re | or send an | EMBL; X56127; | TatorDro: | InterPro; IPR001255; Beta-Al | Pfam; PF03 | | Glycoprofein: | NON_TER | CHAIN | DOMAIN | TRANSMEM
NON TER | SEQUENCE | Ouery Match | Best Local Sin
Matches 8; |
| RESULT
A4_PIG
ID A | AC
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00 | ပ ဒ | RN | RP | Z X | RA | RT | RT | 당 | 3 8 | ဗ | ဥ၂ | 9 5 | 88 | ပ္ပင္ | 38 | ႘ | 8 | 38 | DR | ž | DR CR | DR | DR | X 3 | FT | FF | T | FF | SO | no | Ве |

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SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 VGSNKGAI 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VGSNKGAI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
030-MAY-2000 (Rel. 39, Last annotation update)
Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment)
                                                                                                                                                                                                                                                                 Johnstone E.M., Chaney W.O., Norris F.H., Pascual R., Little S.P., "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species bolymerase chain reaction analysis."; which could be conserved in the conservation analysis."; PURCTION. Brain Res. 10:299-305(1991).

-I. FUNCTION. EUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

-I. SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                        Ursus maritimus (Polar bear) (Thalarctos maritimus).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
NCBL_TaxID=29073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BETA-AMYLOID PROTEIN (POTENTIAL). EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 57; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84209D88EBA82DFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transmembrane.
NOW.TER
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Last annotation update)
                                                                                57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                        MEDLINE=92017079; PubMed=1656157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001868; A4_APP.
InterPro; IPR001255; Beta-APP.
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01-NOV-1997 (Rel. 35, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X56128; CAA39593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03494; Beta-APP; 1
                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1BA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 AA;
             1111111
29 VGSNKGAI 36
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2 VGSNKGAI
                                                                              A4_URSMA
Q29149;
01-NOV-1997 (
01-NOV-1997 (
                                                                                                                                                                                                                                             TISSUE=Brain;
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SEQUENCE
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Q28280;
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                                                         RESULT 2
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A4_CANFA
                                                                       A4_URSMA
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Alzheimer's disease amyloid A4 protein homolog (Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein homolog (Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."; Brain Res. Mol. Brain Res. 10:299-305(1991).

-I. FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLUAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Sukaryota i Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA-AMYLOID PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 BETA-AMALULAR (POTENTIAL).
34 EXTRACELLULAR (POTENTIAL).
58 POTENTIAL.
58 8469D488A2E12DFA CRC64;
7 6285 MW; 8469D488A2E12DFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G(0) (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1;
Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                         MEDLINE-92017079; PubMed-1656157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92017079; PubMed=1656157;
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0
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InterPro; IPR001255; Beta-APP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.4%; 5
100.0%;
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                                                                                           Canis familiaris (Dog).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                            Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P., "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).
-i- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA-AMYLOID PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 1; Length 58;
Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 BETA-AMYLOID PROTEIN (PC
33 EXTRACELLULAR (POTENTIAL)
57 POTENTIAL.
58 CYTOPLASMIC (POTENTIAL).
58 6300 MW; F434209D88EBBAB2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G(0) (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001868; A4_APP.
InterPro; IPR001255; Beta-APP.
                                                                                                                                                                                                                                                                                                                    EMBL; X56129; CAA39594.1; -.
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Best Local Similarity 100.00
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      ; 1BA4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 VGSNKGAI 36
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                                                                                                                                                                                                                                                                                                                                        P05067
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Q28757;
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SEQUENCE
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                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alzhelmer's disease amyloid A4 protein homolog (Contains: Beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE-92017079; PubMed=1656157;
Mohnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
Plan Res. Mol. Brain Res. 10:299-305(1991).
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) EN SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) EN SIGNALING PATHWAY THROUGH THE SIGNALING PROTEIN G(O) EN SIGNALING PROFEIN.
-: SIMELARITY: BELONGS TO THE APP FAMILY.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA-AMYLOID PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1; Length 58; Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                             Pfam: PF03494; Beta-APP; 1.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transmembrane.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
33
57
>58
58
6300 MW;
                                                                                                                                                                                                                                                  EMBL; X56130; CAA39595.1; -. HSSP; P05067; 1BA4.
                                                                                                                                                                                                                                                                                                             InterPro; IPR001868; A4_APP.
InterPro; IPR001255; Beta-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
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Q28053;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1-SUGCELLUAR LOCATION: Type I membrane protein.
-1-DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA, THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXX MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORITATION (BY SIMILARITY).
-1-SIMILARITY: BELONGS TO THE APP FAMILY.
-1-SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
NCBI_TaxID=9521;
                                                                                                                                                                                                                                                                         Gaps
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TISSUE-LIVET, and Kidney;

MEDLINE-96108492; Pubmed-8532114;

LEVY E., Amorim A., Frangione B., Walker L.C.;

"Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid anglopathy."

Neurobiol. Aging 16:805-808(195).

-I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GIP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DBC-1998 (Rel. 37, Last sequence update)
Le-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
                                                                                                                                                                                                                                                                       ;
                                                                                                                               BETA-AMYLOID PROTEIN (POTENTIAL). EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                          Length 59;
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                        F43469D488A2E12D CRC64;
HSSP; P05067; IBA4.

InterPro; IPR01868; A4_APP.
InterPro; IPR001255; Beta APP.
Pfan; PF03494; Beta APP. 1.
PROSITE; PS00319; A4_EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Glycoprotein; Amyloid; Neurone; Transmembrane.
NON TER 7 49 BETA-AMYLOID PROTEIN
                                                                                                                                                                                                                                     68.4%; Score 39; DB 1;
100.0%; Pred. No. 0.82;
ive 0; Mismatches
                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001255; Beta-APP.
InterPro; IPR00223; Kunitz_BFTI.
Pfam; PF00014; Kunitz_BPTI; 1.
Pfam; PF02177; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
                                                                                                                                                                                                       6414 MW;
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                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                       59 AA;
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PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS50279; BPTI_KUNITZ_2; 1.
Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A4_HUMAN STANDARD, PRT, 770 AA. PSG057; PO0605, Q16011; P05067; PO06067, Q16011; P05067; PO0607; Q16011; P05067; P07061-1987 (Rel. 20, created) Q1-NOV-1991 (Rel. 20, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) (Contains: Beta-amyloid protein (Beta-APP) (A-beta)]. APP OR A4 OR CVAP OR ADI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kang J., Lemaire H. G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B., "The precursor of Alzhelmer's disease amyloid A4 protein resembles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        CLATHRIN-BINDING (BY SIMILARITY).
REACTIVE BOND.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-88122639; PubMed-2893289;
Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
Cordell B.;
                                                                                                                                                                                                                                                   BETA-AMYLOID PROTEIN (POTENTIAL). EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (PROBABLE)
N-LINKED (GLCNAC. .) (PROBABLE)
6C3E431089569049 CRC64;
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Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A new A4 amyloid mRNA contains a domain homologous to serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 751; Pred, No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL). BPTI/KUNITZ INHIBITOR.
                                                                                                                                                                                                                     BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                            POTENTIAL.
Pfam; PF03494; Beta-APP; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASTCPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
                                                                                                                                                                                                    protease inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84893 MW;
                                                                       SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KU; 1.
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Nature 331:525-527(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell-surface receptor."; Nature 325:733-736(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    751 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SITE
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"Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.";
Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
                                                                                                                                                                    "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus."; Nucleic Acids Res. 25:1802-1808(1997).
Unterbeck A., Beyreuther K., Mueller-Hill B.; "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons."; Nucleic Acids Res. 17:517-522(1989).
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"A cDNA specifying the human amyloid beta precursor protein (ABPP) encodes a 95-kDa polypeptide.";
Nucleic Acids Res. 16:9351-9351(1988).
                                                                                                                                                                                                                                                                      MEDLINE-88122640; PubMed-2893290;

Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,

Gusella J.F., Neve R.L.;

"Protease inhibitor domain encoded by an amyloid protein precursor

mRNA associated with Alzheimer's disease.";

Nature 331:528-530(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87231971; PubMed=3035574;
Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
"Monecular cloning and characterization of a cDNA encoding the
"erebrowscular and the neuritic plaque amyloid peptides.";
Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
                                                                                                                                  Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
Saito M., Tsukuni S., Sakaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H., "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity."; disease anyloid protein shows nature 31:530-532(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88122641; PubMed=2893291;
                                                                                                                      MEDLINE=97263807; PubMed=9108164;
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Alzheimer's amyloid beta-protein precursor.";
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                                                                                                                                 the Kunitz domain is protease nexin·II.";
Nature 341:144-147(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99215582; PubMed=10201399;
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MEDLINE=92031488; PubMed=1718421;
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MEDLINE=870 J. Weldenan A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
"Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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'Complementary DNA for the mouse homolog of the human amyloid beta
orotein precursor.";
Poulsen S.-A., Watson A.A., Craik D.J., "Solution structures in aqueous SDS micelles of two amyloid beta peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
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16-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein homolog precursor
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                                              Struct. Biol. 130:142-152(2000).
                                                                                                                               water.";
J. Struct. Biol. 130:130-141(2000).
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MEDLINE=89345111; PubMed=2569710;
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                                                                     STRUCTURE BY NMR OF 681-706
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WITH X11-ALPHA, -BETA, AND -GAMAA, THE ENDURENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
NPXY MOTIF THIS INTERACTION APPEARS TO BE INDEPENDENT OF
PHOSPHORYLATION (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE APP FAMILY.

-1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                 "Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse."; Gene 112:189-195(1992).
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MEDLINE-89149813; PubMed-2493250;
WEDLINE-89149813; PubMed-2493250;
"Samada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
"Structure and expression of the alternatively-spliced forms of mRNA for the mouse homolog of Alzheimer's disease amyloid beta protein
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TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 158:906-912(1989).
--- SUBCELUJAR LOCATION: Type I membrane protein.
--- ALTERNATIVE PRODUCTS: 5 ISOPRMS; APP(395), APP(563), APP(695),
APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
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SEQUENCE OF 1-19 FROM N.A.
MEDLINE-92209998; PubMed-1555768;
Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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PROSITE; PS00320; Ad_INTRA; 1.
PROSITE; PS00280; BPTL_KUNIT2.1; 1.
PROSITE; PS50279; BPTL_KUNIT2.2; 1.
GlyCoprotein; Amyloid; Neurone; Transmembrane; Signal;
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EMBL; M18373; AAA37139_1; -
EMBL; X15210; CAA33280_1; -
EMBL; D10603; BAA01456_1; -
EMBL; M24397; AAA3959_1; -.
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InterPro; IPR001868; A4_APP.
InterPro; IPR001255; Beta-APP.
InterPro; IPR001223; Kunitz_BPTI.
Pfam; PF0014; Kunitz_BPTI: 1.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PR03494; Beta-APP; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
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PIR, S04855; S04855.
PIR, S19727; S19727.
HSSP; P05067; 1AAP.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between, the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- SIMILARITY: BELONGS TO THE APP FAMILY.

-i- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                              Gaps
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Kang J., Mueller-Hill B.;

"The sequence of the two extra exons in rat preA4.";

Nucleic Acids Res. 17:2130-2130(1989).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(695),

APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seeburg P.H.; "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact."; EMBO J. 7:1365-1370(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
                 CLATHRIN'BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
E -> V (IN ISOFORM APP(695)).
MISSING (IN ISOFORM APP(695)).
MISSING (IN ISOFORM APP(751)).
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Pred. No. 9.3;
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01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein homolog precursor
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     BPTI/KUNITZ INHIBITOR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=88312583; PubMed=2900758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Amyloidogenic glycoprotein) (AG)
                                                                                                                                                                                      86752 MW;
                                                                                                                                                                                                                          68.4%; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 289-364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X07648; CAA30488.1; -. EMBL; X14066; CAA32229.1; -.
                                                                                                                                                                                                                      Query Match 68.4
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
     345
762
3341
334
337
542
571
364
364
380
 287
759
300
316
542
571
289
299
290
346
                                                                                                                                                                                                                                                                                                                      695 VGSNKGAI 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                 2 VGSNKGAI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLICING
                        SITE
DISULFID
                                                         DISULFID
                                                                                                                                                    VARSPLIC
VARSPLIC
                                                                                             CARBOHYD
                                                                                                              CARBOHYD
                                                                                                                                                                                      SEQUENCE
                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                            A4_RAT
P08592;
     DOMAIN
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A4_RAT
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLIND-9804934; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rèl. 40, Last annotation update)
Probable adenine deaminase (EC 3.5.4.2) (Adenase) (Adenine aminase).
                                                                                                                                                                                                                                                                                                                                                                                                       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPTI/KUNITZ INHIBITOR.
CLATHRIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> V (IN ISOFORM APP(695)).
MISSING (IN ISOFORM APP(695)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EQUIVALENT OF BETA-AMYLOID PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%; Score 39; DB 1; Length 770; 100.0%; Pred. No. 9.3; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   SMART; SM00131; KU; 1.

PROSITE; PS00130; A4_INTRA; 1.

PROSITE; PS00320; A4_INTRA; 1.

PROSITE; PS50279; BPTI_KUNITZ_1; 1.

PROSITE; PS50279; BPTI_KUNITZ_2; 1.

Glycoprotein; Amyloid; Neurone; Transmembrane; Signal; Alternative spliting; Serine protease inhibitor.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C26C9D6BB2D929A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                   Pfam; PF00014; Kunitz_BPT1; 1. Pfam; PF02177; A4_EXTRA; 1. Pfam; PF03494; Beta_APP; 1. PRINTS; PR00203; AMYLOIDA4. PRINTS; PR00759; BASTCPTASE. ProDom; PD000222; Kunitz_BPT1; 1. SMART; SM0006; A4_EXTRA; 1.
HSSP, P05067; JAAP.
InterPro; IPR001868; A4_APP.
InterPro; IPR001255; Beta-APP.
InterPro; IPR002223; Kunitz_BPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VGSNKGAI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADEC_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
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ADEC_ARCFU
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modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary;
MEDLINE=99413504; PubMed=10485494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLK8 OR PRSS19 OR TADG14 OR NRPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                             EMBL; AE000845; AAB85151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                               474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 213:9-16(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 CIGIKKGFLC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CVGSNKGAIC 10
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein)
                                                                                                                                                                                                                                                                                                                 CHAIN
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       á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-glutamate - L-glutamine + 5-phospho-alpha-D-ribose 1-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98037514; pubMed-9371463; Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qlu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum GeltaH; functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: De novo purine biosynthesis; first step.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
-!- SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amidophosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPATase).
                                     hyperthermophilic, sulphate-
                                                                                       -i- CATALYTIC ACTIVITY: Adenine + H(2)O = hypoxanthine + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 556; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGR01178; ade; 1.

Hypothetical protein; Hydrolase; Complete proteome.

SEQUENCE 556 AA; 60764 MW; B3E3440A09F86A79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 AA.
                                                        reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                     "The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR002832; Adenine_deam.
Pfam; PF01979; Adenine_deam; 1.
                                                                                                                                                                                                                                                                                        EMBL; AE001089; AAB90993.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                       64.9%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 CVGVDDGSIC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVGSNKGAIC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PURF OR MTH646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUR1_METTH
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PUR1_METTH
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Usage by and for commercial
                  (See http://www.isb-sib.ch/announce/
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060252, Q90QAT, Q9HCB3; Q9UIL9;
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
15-JUL-2002 (Rel. 41, Last annotation update)
Neuropsin precursor (EC 3.4.21.~) (NP) (Kallikrein 8) (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Brien T.J.;
"Cloning of tumor-associated differentially expressed gene-14, a novel
serine protease overexpressed by ovarian carcinoma.";
Cancer Res. 59:4435-4439(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-98372070; PubMed-9714609; Yoshida S.; Taniguchi M., Hirata A., Shiosaka S.; "Sequence analysis and expression of human neuropsin cDNA and gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.; "A novel form of human neuropsin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY. AMIDOPHOSPHORIBOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 36; DB 1; Length 474; 50.0%; Pred. No. 22; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;
                                                                                                                                                                                                        TICRFAMS; TIGNOL134; PULF; 1.

PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.

PROSITE; PS00443; GATASE_TYPE_II; 1.

Purine biosynthesis; Transferase; Givcosyltransferase;
Glutamine amidotransferase; Complete proteome.

100
                                                                                                                                                                                                                                                                                                                                                                                  11 11 GATASE (BY SIMILARITY).
474 AA; 52660 MW; 16BAF93BBF15A0D2 CRC64;
                                                                                                                     InterPro; IPR000583; GATase_2.
InterPro; IPR000836; PRTransferase.
InterPro; IPR002375; Pr/py_rp_transf.
Pfam; PF00156; Pribosyltran; I.
Pfam; PF00310; GATase_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 260:627-634(1999).
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Bhan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;

Seduntated (OCT-2000) to the EMBL/Genbank/DDBJ databases.

-: FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIPPOCAMPAL PLASTICLTY.

-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.

-!- SUBCELLULAR LOCATION: Secreted.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
"Molecular cloning and characterization of a novel serine protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                              MEDILINE-2010030; PubMed-11054574;

MEDILINE-2010030; PubMed-11054574;

Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,

Moss P., Paeper B., Wang K.;

"Sequencing and expression analysis of the serine protease gene

cluster located in chromosome 19q13 region.";
                         ovasin, a potential molecular marker for ovarian carcinomas.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGNINE PEO0089; LTYPSIN; I.
PRINTS: PRO0721; CHYMOTRYPSIN.
PRART; SM00020; TTYP_SPC; I.
PROSITE; PS50240; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_HIS; I.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM (BY
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InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB009849; BAA28673.1; --
EMBL; AB012761; BAA28676.1; --
EMBL; AB010780; BAA88676.1; --
EMBL; AB008990; BAA82665.1; --
EMBL; AB008927; BAA8266.1; --
EMBL; AF095742; AAD56050.1; --
EMBL; AF095742; AAD55979.1; --
EMBL; AF095743; AAD33861.1; --
EMBL; AC01473; AAG33361.1; --
EMBL; AC01473; AAG3354.1; --
EMBL; AC01474; AAG3354.1; --
EMBL; AC01474; AAG3354.1; --
EMBL; AC01474; AAG3554.1; --
EMBL; AC01474; AAG3544.1; --
EMBL; AC01474; AAG3544.1; --
EMBL; AC01474; AAG3544.1; --
EMBL; AC01474; AAG3544.1; --
EMBL; AC01474; AAG35
                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIPPOCAMPAL PLASTICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.244; -- Genew; HGNC:6369; KLK8.
                                                                                                                                                                                                                                                                                                         Gene 257:119-130(2000).
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BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

A >> AGGGELLITYERARLIACVHINPOWPSQPSHCPRG
WWS.RELPPAA (IN ISOPORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2001 (Rel. 40, Last annotation update)
Adhesive plaque matrix protein 2 precursor (Foot protein 2) (MGFP2)
(MGFP-2).
                                                                                                                                                                                                                                                                                                                           Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytilolda;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=29158;
                                                                                                                                             ö
                                                                                                                      Score 35; DB 1; Length 260;
Pred. No. 19;
                                                                                                                                             1; Indels
                                                                                                                                                                                                                                            473 AA.
                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00010; ASX_HYDROXXL; 2. PROSITE; PS00022; EGF_1; 11. PROSITE; PS01186; EGF_2; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00740; IEDM.
InterPor; IPR000152; Asx hydroxyl.
InterPor; IPR000561; EGF-like.
InterPor; IPR000742; EGF_2.
InterPro; IPR01881; EGF_Ca.
Pfam; PF00008; EGF; 11.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95204464; PubMed-7896812;
                                                                                                   28048 MW;
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                                                                                                                         61.4%;
75.0%;
                                                                                                                                   Best_Local Similarity 75.0
Matches 6; Conservative
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  173
74
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                                                                                                   260 AA;
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Q25464;
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                            ACHESIVE PLAQUE MATRIX PROTEIN 2.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 9.
EGF-LIKE 9.
EGF-LIKE 10.
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    domain; Repeat; Signal; Hydroxylation.
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 Glycoprotein; EGF-like SIGNAL 17
                              387
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473 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                              SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed-9923682;
ALD R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noona B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                                                                                           "IF FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway (By similarity).
-!-CATALKITIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
-!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                 "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.6%; Score 34; DB 1; Length 316; 100.0%; Pred. No. 35; 0; Indels ive 0; Mismatches 0; Indels
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ACT_SITE 127 127 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001561; AAD06969.1; -.
InterPro; IPR004732; Tal_mycobact.
InterPro; IPR001585; Transaldolase.
Pfam. PF00923; Transaldolase.
TIGRRAMS; TIGR00876; tal_mycobact; 1.
PROSITE; PS01054; TRANSALDOLASE_1; 1.
PROSITE; PS00958; TRANSALDOLASE_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 127 B
316 AA; 35340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                    Helicobacter.
NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 NKGAIC 10
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SEQUENCE
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Search completed: November 9, 2002, 14:01:43 Job time: 8.69231 secs

Helicobacter pylori J99 (Campylobacter pylori J99).

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 9, 2002, 13:59:34; Search time 13.8462 Seconds (without alignments) 69.430 Million cell updates/sec Run on:

US-09-632-748-4 57 1 CVGSNKGAIC 10 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | dР | | | SUMMARIES | |
|---------------|-------|-------|-----------------------|----|-----------|--------------------|
| Result
No. | Score | Query | Query
Match Length | 80 | ID | Description |
| 1 | 40 | 70.2 | 284 | 7 | F82666 | phage-related prot |
| 7 | 39 | 68.4 | 42 | 7 | PN0512 | Ω |
| m | 39 | 68.4 | 57 | 7 | E60045 | ਾ |
| 4 | 39 | 68.4 | 57 | 7 | F60045 | ďį |
| Ω | 39 | 68.4 | 57 | ~ | G60045 | |
| 9 | 39 | 68.4 | 57 | 7 | D60045 | Alzheimer's diseas |
| 7 | 39 | 68.4 | 57 | 7 | A60045 | Alzheimer's diseas |
| æ | 39 | 68.4 | 57 | 7 | B60045 | Alzheimer's diseas |
| O | 39 | 68.4 | 82 | 7 | PQ0438 | Alzheimer's diseas |
| 10 | 39 | 68.4 | 695 | 7 | A49795 | Alzheimer's diseas |
| 11 | 39 | 68.4 | 695 | 7 | A27485 | ß |
| 12 | 39 | 68.4 | 695 | 7 | 800550 | Alzheimer's diseas |
| 13 | 39 | 68.4 | 747 | ~ | JH0773 | Alzheimer's diseas |
| 14 | 39 | 68.4 | 770 | - | QRHUA4 | Alzheimer's diseas |
| 15 | 38 | | 372 | 7 | T29359 | hypothetical prote |
| 16 | 37 | | 83 | 7 | T22622 | |
| 17 | 37 | 64.9 | 256 | 7 | Н69279 | ╌ |
| 18 | 36 | 63.2 | 474 | 7 | H69185 | amidophosphoribosy |
| 19 | 36 | 63.2 | 1088 | 7 | A69493 | cysteine proteinas |
| 20 | 36 | 63.2 | 1555 | 7 | T18688 | hypothetical prote |
| 21 | 36 | 63.2 | 1973 | 7 | 689608 | $^{\sim}$ |
| 22 | 36 | 63.2 | 1973 | 2 | T18686 | hypothetical prote |
| 73 | 35 | 61.4 | 299 | 7 | F95294 | 24 |
| 24 | 35 | | 473 | ~ | A56175 | adhesive plaque pr |
| 25 | 35 | ä | 786 | 7 | ന | single-strand DNA- |
| 56 | 34 | 9. | 87 | 7 | 72 | transferrin - shee |
| 27 | 34 | 59.6 | 191 | 7 | 95 | hypothetical prote |
| 28 | 34 | e, | 191 | ~ | T22036 | |
| 29 | 34 | 6 | 316 | ~ | 0 | Ψ |

| transaldolase - He | | histidine-tRNA lig | hypothetical prote | hypothetical prote | | hypothetical prote | hypothetical prote | phosphoprotein pho | hypothetical prote | methyl-accepting c | hypothetical prote | probable DNA-direc | hypothetical prote | nucleoporin - fiss |
|--------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| E71812
T22998 | T51506 | G70116 | T45816 | S76211 | T20839 | T19346 | B71409 | A42287 | T42754 | AD2076 | T52516 | 528103 | T20406 | T43682 |
| ~ ~ | 1 7 | ~4 | 7 | ~ | 7 | N | ~ | Н | 7 | ~ | 7 | ~ | 7 | 7 |
| 316 | 426 | 457 | 470 | 611 | 615 | 640 | 644 | 661 | 661 | 752 | 795 | 797 | 1391 | 1628 |
| ب ب | 9 | 9. | 9. | 9. | 9. | 9. | 9. | 9. | 9. | 9. | ७. | 9. | 9. | 9. |
| 59.6 | 59 | 59 | 59 | 59 | 59 | 59 | 59 | 59 | 5 | 59 | 59 | 29 | 59 | 29 |
| 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| 30 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| | XF155 |
|---|----------|
| | protein |
| | -related |
| 9 | - 1 |

5 [imported] - Xylella fastidiosa (strain 9a5c)

Cispecies: Xylella fastidiosa
Cispecies: Yylella fastidiosa
Cispec

A; Gene: XF1555 C; Genetics:

Query Match

Gaps ö 70.2%; Score 40; DB 2; Length 284; 60.0%; Pred. No. 7.3; 2; Indels 2; Mismatches Best_Local Similarity 60.0 Matches 6; Conservative

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1 CVGSNKGAIC 10 á

248 CVGDDDGALC 257 Db

PN0512

Deta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Species: 31-pec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PNO51: PNO51: Anstamoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno B;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

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C; Accession: G60045
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                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-bec-1992 #sequence_revision 01-bec-1992 #text_change 28-Jul-1995
C;Date: 01-bec-1992 #sequence_revision 01-bec-1992 #text_change 28-Jul-1995
C;Datesion: EG0045
R;Johnstone, E.M; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, A;Reference number: A60045; MUID:92017079; PMID:1656157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C; Accession: F60045
R; Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, A; Reference number: A60045; MUID:92017079; PMID:1656157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-57 
A; Residues: 1-57 
A; Cross-references: EMBL: X56130
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase C; Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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A; Residues: 1-57 < CODH:
A; Cross-references: EMBL:X56127; NID:91895; PIDN:CAA39592.1; PID:91896
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C; Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
                                            A; Molecule type: protein
A; Realdues: 1-42 csHr.
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C; Keywords: alternative splicing; amyloid
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C;Dafe: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
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A; Reference number: PN0512; MUID: 93290653; PMID: 7685598
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2.6;
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100.0%; Pred. No. ...
0; Mismatches
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Conservative 0; Mismatches
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29 VGSNKGAI 36
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29 VGSNKGAI 36
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A,Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <-JOHN
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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C;Species: Canis lupus familiaris (dog)
C;Species: Calis lupus familiaris (dog)
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Fille: Conservation of the sequence of the Alzheimer's disease amyloid peptide in A;Reference number: A60045; MUID:92017079; PMID:1656157
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R. Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A.; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in A; Reference number: A60045; MUID:92017079; PMID:1656157
Cyncuscing and the sequence of the Alzheimer's disease amyloid peptide. A; Nohestone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P. Brain Res. Mol. Brain Res. 10, 299-305, 1991
A; Fitle: Conservation of the sequence of the Alzheimer's disease amyloid peptide. A; Reference number: A60045; MUID:92017079; PMID:1656157
A; Accession: G60045
A; Molecule type: mRNA
A; Residues: 1-57 < JOHA
A; Cross-references: EMBL:X56126
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote C; Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal
C;Keywords: alternative splicing; Alzheimer's disease; amyloid;
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100.0%; Pred. No. 2.6;
iive 0; Mismatches
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Best Local Similarity 100.00
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Best Local Similarity 100.
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es 8; Conserv
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A; Status: translated from GB/EMBL/DDBJ
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N'Alternate names: proteinase nexin
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Best Local Similarity luv...
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Matches 8; Conservative
            A; Residues: 1-695 <POD>
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                                                                           C; Species: Ursus martinus (polar bear)
C; Species: Ursus martinus (polar bear)
C; Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C; Accession: B660045
R; Johnstone, E. M.; Chaney, M.O.; Norris, F. H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, A; Accession: B60045, MUID: 92017079; PMID: 1656157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Accession: P00438
A. Molecule type: DNA
A. Residues: 1-82 < DAV>
A. Cross-references: GB: M83558; GB: M83657
R. Johnstone, E. M.; Chaney, M.O.; Norris, F. H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A. Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, A; Reference number: A60045; MUID: 92017079; PMID: 1656157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C; Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C; Accession: P00438; C60045
R; Davidson, J.S; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A; Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor A; Reference number: P00438; MUID:93075180; PMID:1445331
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome
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                                                   Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
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Matches 8; Conserv
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A; Residues: 12-68 <JOH>
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RESULT 8
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A; Molecule type: mRNA
A; Residues: 1-210, /G', 212-220, /S', 222-396, /A', 398-402, /T', 404-448, /A', 450-695 <STR>
A; Residues: 1-210, /G', 212-220, /S', 222-396, /A', 398-402, /T', 404-448, /A', 450-695 <STR>
A; Cross-references: EMBL: X59379
R; Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A; Title: Positive and negative regulatory elements for the expression of the Alzheime
A; Reference number: 149485; MUID: 92209998; PMID: 1555768
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C;Keywords: alternative splicing
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change.13-Aug-1999
C;Accession: A27485; $19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr A;Reference number: A27485; MUID:88106489; PMID:3322280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: brain R; van den Berghe, H.
R; de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A; Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos A; Reference number: $19727; MUID: 92096458; PMID: 1756177
A; Accession: $19727
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N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A38820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br
A;Reference number: S00550; MUID:88312583; PMID:2900758
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A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
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100.0%; Pred. No. 26;
iive 0; Mismatches
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Pred. No. 26;
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100.0%; Pred. No. 26;
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protein precursor splice form APP(770)

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A; Accession: located acid sequence not shown; translation not shown; translated from GB/A; Molecule type: DNA
A; Wolecule type: DNA
A; Rolecule type: DNA
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A; Residues: 1-14, VW', 17-288, V', 365-770 < LEM2>
A; Residues: 1-14, VW', 17-288, V', 365-770 < LEM2>
A; Residues: 1-14, VW', 17-288, V', 365-770 < LEM2>
A; Coss references: EMBL:X1466; NID:935599; PIDN:CAA31830.1; PID:9871360
A; Note: alternative splice form APP(695)
B; La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem Biophys. Res. Commun. 159, 297-304, 1989
A; Title: Characterization of the 5'-end region and the first two exons of the beta-pr A; Reference number: A32277; MUD:89165870; PMID:2538123
A; Reference number: A32277; MUD:89165870; PMID:2538123
A; Residues: 1-75 < LAF>
A; Coss-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AAC13654.1; PID:9516074
A; Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN
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A; Residues: 656-737 4.00H>
A; Residues: 656-737 4.00H>
B; R; Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
Biochen. Biophys. Res. Commun. 170, 301-307, 1990
A; Fitle: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A; Reference number: A35486; MUID:90331244; PMID:2196878
C; Species: Homo sapiens (man)
C; Date: 30-Unu-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C; Date: 30-Unu-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C; Date: 30-Unu-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C; Accession: S02260; S05194; A32277; A33260; A33486; 139452; 139453; 139453; 139453; 159562; A668; A28583; A28583; A29302; A6085; Julhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Nucleic Acids Res. 17, 517-522, 1989
A; Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode A; Reference number: S02260; MuID:89128427; PMID:2783775
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A;Status; nucleic acid sequence not shown; translation not shown; translated from GB/
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A; Residues: 672-710 (PREI>
A; Note: 693-Gln was found in DNA isolated from HCHWA-D patients
A; Note: 63-Gln was found in DNA isolated from H.; Sakaki, Y.
R; Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A; Title: Genomic organization of the human amyloid beta-protein precursor gene.
A; Reference number: 139451; MUID:90236318; PMID:2110105
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A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
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A; Residues: 1-288, V',365-770 <LEMI>
A; Cross-references: EMBL:X13466
A; Note: alternative splice form APP(695)
R; Lemaire, H.G.
Submitted to the EMBL Data Library, November 1988
Submitted to the EMBL Data Library, November 1988
A; Reference number: S05194
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A; Residues: 656-737 <LEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G. FEBS Lett. 349, 109-116, 1994
A; Title: The beta-A4 amyloid precursor protein binding to copper.
A; Reference number: $46251; MUID:94320627; PMID:7913895
A; Contents: annotation; copper binding sites
A; Note: rat peptides were isolated but not sequenced
A; Note: rat peptides were isolated but not sequenced
A; Note: rat peptides, J; Mehta, P.; Kim, K.S.; Miller, D.L.
J Biol. Chem. 266, 8464-8469, 1991
A; Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain A; Reference number: A39820; MUID:91217087; PMID:1673681
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A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
                                                                                      A;Cross-references: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617
A;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitch, T.; Cole, G.
Sclence 241, 233-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
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C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPL>
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C; Superfamily: Alzheimer's disease amyloid bete protein; animal Kunitz-type proteinses
C; Keywords: alternative splicing; amyloid; qlycoprotein; transmembrane protein
F; 625-648/Domain: transmembrane #status predicted <TMM>
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Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
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A; Experimental source: brain
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Best Local Similarity
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Molecule type: protein
Residues: 18-32 <POT>
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A; Residues: 1-747 <OKA>
           A; Molecule type: mRNA
A; Residues: 1-695 <SHI>
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QRHUA4
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A; Molecule type: mRNA
A; Residues: 287-367 (4872-
A; Residues: 287-367 (4872-
A; Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9929611
A; Experimental source: glioblastoma cell line
A; Experimental source: glioblastoma cell line
A; Note: alternative splice form APP(770)
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A; Fitle: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre A; Reference number: A30320
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A; Residues: 606-770 «VIT3>
R; Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A; Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A; Reference number: A31087; MUID:88124954; PMID:2893379
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A;Residues: 507-770 C2AI>
A;Cross-references: GB:MB0334; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
B as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther,
                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhi A;Reference number: $00925; MUID:88122639; PMID:2893289
A;Accession: $00925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-344, "I', 365-770 <PO2>
A; Cross-references: GB: X06989; EMBL: Y00297; NID: 928720; PIDN: CAA30050.1; PID: 928721
A; Orce: alternative splice form APP(751)
A; Note: alternative splice form APP(751)
Nature 331, 530-532, 1988
A; Titler Novel precursor of Alzheimer's disease amyloid protein shows protease inhib1
A; Titler Novel precursor of Alzheimer's disease amyloid protein shows protease inhib1
A; Reference number: A38949; MUID: 88122641; PMID: 2893291
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
                                                                                                                                                                                                                                                                                                                                                        D.; Greenberg,
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C;Species: Caenorhabditis elegans
C;Species: Lact-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29359
R;Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
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red. No. 28;
Mismatches 0; Indels
                                                                                                                                         A; Molecule type: mRNA
A; Residues: 286-344, Tr,365-366 < TAN2>
A; Cross-references: EMBL: X06982; NID:928817; PIDN: CAA30042.1;
A; Experimental source: promyelocytic leukemia cell line HL60
A; Note: alternative splice form APP(751)
A; Flonte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.;
Nature 331, 525-527, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 122-288,'V',365-770 <VIT2> A;Accession: C30320
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Pred. No.
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100.0%; Pre
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les 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Molecule type: NA
A.Cross-references: 689-716, 'F', 718-737 < MUD:
A.Cross-references: 685-7665; NID: 9236721
B.Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, Am. J. Hum. Genet. 51, 998-1014, 1992
A.Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the A.Recession: A44017; MUID: 93035397; PMID: 1415269
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R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve Nature 331, 528-530, 1988
    A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
A;Note: a mutation with 693-Gln is presented
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheime
A;Reference number: I59562; MUID:92022553; PMID:1925564
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A; Residues: 284-288, V',365-646, E',648-770 <ROB>
A; Cross-references: GB:MI0765; NID:g178539; PIDN:A451722.1; PID:g178540
A; Note: the authors translated the codon GAG for residue 647 as Asp
R; Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A; Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A; Reference number: A47584; MUID:87120328; PMID:3810169
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A;Reference number: A03134; MUID:87144572; PMID:2881207
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A;Reference number: SO2638; MUID:88296437; PMID:2900137
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Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
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A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
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A;Residues: 687-692,'G',694-718 <KAM1>
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
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A; Residues: 687-718 <KAMZ>
A; Residues: 687-718 <KAMZ>
A; Cross-references: GB:845136; NID:9257379; PIDN:AAB23646.1; PID:9257380
A; Cross-reference: familial Alzhelmer disease family LIT
A; Note: sequence extracted from NCBI backbone (NCBIP:115376)
A; Note: this sequence has a silent mutation
B; Kang, J; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; CNature 325, 733-736, 1987
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A;Residues: 674-756,'S.',758-770 <GOL>
A;Cross-references: GB:M1553; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
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A.Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A.Note: alternative splice form APP(695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                  Accession: I59562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A03134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A47584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S02638
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A; Description: The sequence of C. elegans cosmid R05G6.
A; Reference number: 220612
A; Accession: T29359
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-372 < MUR>
A; Residues: 1-372 < MUR>
A; Experimental source: EMBL:U58746; PIDN:AAB00626.1; GSPDB:GN00022; CESP:R05G6.9
A; Experimental source: strain Bristol N2; clone R05G6
A; Gene: CESP:R05G6.9
A; Map position: 4
A; Introns: 80/1; 161/1; 245/1; 286/1
                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels
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|139 CVGSKKAPLC 148
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OM protein

Run on:

Sequence:

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MULLAN, Michael John
CHARTER-HARLIN, Marie-Christine
OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Pallo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Pred. No. 0.34; 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10025219
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
GOATE, Alison Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111
24 VGSNKGAI 31
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US-10-025-219-1
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LENGTH: 42
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Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
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                                                                                          9, 2002, 14:01:49; Search time 4.23077 Seconds (without alignments) 26.619 Million cell updates/sec
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Sequence 2, App
Sequence 3, App
Sequence 395, 1
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Sequence 3
Sequence 3
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1: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO8_NEW_COMB.pep:*
             5.1.3
Compugen Ltd.
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US-10-025-219-1

US-10-025-219-2

US-10-025-219-3

US-10-145-087A-395

US-10-145-037A-395

US-10-162-522A-395

US-10-162-522A-395

US-10-165-353-395

US-10-170-481A-395

US-10-170-481A-395

US-10-145-088A-395

US-10-145-088A-395

US-10-145-088A-395

US-10-131-813A-396

US-10-131-824A-396

US-10-131-824A-396

US-10-131-824A-396

US-10-131-824A-396

US-10-131-824A-396

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US-10-131-824A-396
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US-10-127-835A-396
US-10-127-837A-396
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                                                                                                                                                                                                                                                 39427 segs, 11261862 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
           GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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57
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Match Length
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Perfect score:
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Gaps

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0; Indels

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Sequence 1, Application US/10278181
GENERAL INFORMATION:
APPLICANT: Chol/Kier, Mario
APPLICANT: Chol/Kier, Mario
TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
TITLE OF INVENTION: Disease
FILE REPERENCE: CHONTERS 04302
FILE REPERENCE: CHONTERS 04302
CURRENT APPLICATION NUMBER: US/10/278,181
CURRENT PILING DATE: 2002-10-21
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 1.00
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
US-10-127-842A-396
US-10-127-850A-396
US-10-127-901A-396
US-10-128-689A-396
US-10-131-833A-396
US-10-131-833A-396
US-10-127-898-396
US-10-127-898-396
US-10-127-898-396
US-10-128-686A-396
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US-10-131-836A-396
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RESULT 4
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GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: HARDY, Alison Mary
MULLAN, Michael John
CHARTIER-HARLIN, Marie-Christine
OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 695; 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFRENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 326-2400
TELEFAX: (415) 326-2420
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE: 18-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-Jun-1995
                                                                                                                                                                        APPLICATION DATE:

FILING DATE: 05-Jun-1995
APPLICATION NUMBER: 08/104,165
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-AN-1991
FILING DATE: 21-AN-1991
FILING DATE: 28-ANG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.4%; Score 39; DB 100.0%; Pred. No. 5.9
                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,219
FILING DATE: 18-DEC-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                 MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 695 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                             PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94301
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Best Local Similarity
'-haa 8; Conserve
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Gaps
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TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOATE, Alison Mary
MULLAN, Michael John
CHARTIER-HARLIN, Marie-Christine
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 16163-000100 TELECOMMUNICATION INFORMATION: TELEFONE: (415) 326-2400 TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 16163-000100 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.4%; Score 39; DB 6;
100.0%; Pred. No. 6.4;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-Jun-1995
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 918445.7
FILING DATE: 28-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/025,219
FILING DATE: 18-Dec-2001
CLASSIFICATION: CUNROWN>
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-025-219-2
       08/104,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HARDY, John Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10025219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.4 Best Local Similarity 100. Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676 VGSNKGAI 683
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SEQ ID NO 395
LENGTH: 260
                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                       DB 6; Length 770;
6.6;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                       68.4%; Score 39; DB 100.0%; Pred. No. 6.6 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/145,087A CURRENT FILING DATE: 2001-10-18 PRIOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/062250
                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/064249
PRIOR PILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PAPLICATION NUMBER: 60/066364
PRIOR PILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 395, Application US/10145087A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/077641
FILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/077649
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7770 amino acids
TYPE: amino acid
                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Gerber, Hanspeter
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 100.0
Matches 8; Conservative
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Eaton, Dan
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US-10-145-087A-395
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                              Remaining Prior Application data removed – See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
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                                                                                                                                                                                                                                      Length 260;
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Pred. No. 11;
1; Mismatches
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2097-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-110-17
PRIOR FILING DATE: 1997-110-17
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Shelton, David L.
Stewart, Timothy A.
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75.0%;
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Gerber, Hanspeter
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 75.0
Matches 6; Conservative
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Eaton, Dan
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US-10-145-087A-395
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
LENGTH: 260
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11;
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Pred. No. 11;
1; Mismatches
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CURRENT APPLICATION NUMBER: US/10/145,092A
CURRENT FILING DATE: 2002-10-10
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PRIOR FILING DATE: 1997-11-13
PRIOR PILICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR PLICATION NUMBER: 60/077632
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION UNDBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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Shelton, David L.
Stewart, Timothy A.
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75.0%;
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Gao, Wei-Qiang
Gerber, Hanspeter
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Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                           TYPE: PRT
ORGANISM: HOMO Sapiens
US-10-143-031A-395
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198 CAGSSKGA 205
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC56
CURRENT APPLICATION NUMBER: US/10/162,522A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06220
PRIOR PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 395
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Pred. No. 11;
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Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
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; Sequence 395, Application US/10162522A
; GENERAL INFORMATION:
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Shelton, David L.
Stewart, Timothy A.
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75.0%;
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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Hillan, Kenneth J
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Kuo, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 75.0
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-10-145-092A-395
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| 198 CAGSSKGA 205
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 395
LENGTH: 260
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11;
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1; Mismatches
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CURRENT APPLICATION NUMBER: US/10/165,038A
CURRENT FILING DATE: 2007-10-1
                                                                                                                                                                    Score 35;
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                    61.4%;
75.0%;
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-522A-395
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198 CAGSSKGA 205
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APPLICANT:
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunnas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC40
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 395
LENGTH: 260
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Pred. No. 11;
1; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/165,353
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR PELING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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75.0%;
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Filvaroff, Ellen
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Gerritsen, Mary E
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Best Local Similarity 75...
نمر 6; Conservative
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Gao, Wei-Qiang
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US-10-165-038A-395
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SEQ ID NO 395
LENGIH: 260
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                   Gaps
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR PILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
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                                                                                                                                                                                                                         61.4%; Score 35; DB 6; Length 260; 75.0%; Pred. No. 11;
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CURRENT APPLICATION NUMBER: US/10/170,481A
CURRENT FILING DATE: 2002-10-10
PRIOR PILICATION NUMBER: 09/918585
PRIOR PELLING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-33
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PELLING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR PELLCATION NUMBER: 60/065364
PRIOR FILING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLORION NUMBER: 60/065364
PRIOR FILING DATE: 1999-110-13
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Ashkenazi, Avi
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
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                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-165-353-395
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Best Local Similarity
Matches 6; Conserv
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198 CAGSSKGA 205
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                                                                                              SEQ ID NO 395
LENGTH: 260
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILLING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 1097-10-17
PRIOR APPLICATION NUMBER: 60/06429
PRIOR PILING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06534
PRIOR APPLICATION NUMBER: 60/06634
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077631
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-11
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Filvaroff, Ellen
Fong, Sherman
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Kuo, Sophia S.
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Eaton, Dan
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Best Local Similarity
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198 CAGSSKGA 205
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US-10-172-039A-395
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/145,016A

CURRENT FILING DATE: 2001-10-18

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-21

PRIOR PLICATION NUMBER: 60/06534

PRIOR PLICATION NUMBER: 60/065364

PRIOR PLICATION NUMBER: 60/065364

PRIOR FILING DATE: 1997-11-21

PRIOR PLICATION NUMBER: 60/077450

PRIOR PLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 395
LENGTH: 260
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Pred. No. 11;
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1; Mismatches
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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Gerber, Hanspeter
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Best Local Similarity 75.v.
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                                                                                                                                                              ; ORGANISM: Homo sapiens US-10-172-039A-395
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                                                                                                                                                                                                                                                                                                                        198 CAGSSKGA 205
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APPLICANT:
APPLICANT:
                                                                                                                                              TYPE: PRT
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 395
LENGTH: 260
TYPE: PRI
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                                                                                                                                                                                                                                       Score 35; DB 6; Length 260;
Pred. No. 11;
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PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06531
PRIOR APPLICATION NUMBER: 60/06531
PRIOR PILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06546
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 395, Application US/10145088A, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Wood, William I.
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
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Shelton, David L.
Stewart, Timothy A.
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Fong, Sherman
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity 75.v.
5.conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumas, Daniel
                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-145-016A-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton, Dan
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198 CAGSSKGA 205
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US-10-145-088A-395
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                                                                                                                                                                                                                                                                                    Gaps
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
ESEQ ID NO 395
LENGTH: 260
                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                    61.4%; Score 35; DB 6; Length 260; 75.0%; Pred. No. 11; ° 1; Indels Live 1; Mismatches 1; Indels
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PRIOR PAPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2010-07-30
PRIOR APPLICATION NUMBER: 60/06220
PRIOR APPLICATION NUMBER: 60/06424
PRIOR APPLICATION NUMBER: 60/06431
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065314
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07750
PRIOR APPLICATION NUMBER: 60/07750
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PELING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR PELING DATE: 1998-03-11
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Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 395, Application US/10145129A
GENERAL INFORMATION:
APPLICANT: Ashkonazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                              Query Match
Best Local Similarity 75.۰
امار و Gi Conservative
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-088A-395
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198 CAGSSKGA 205
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US-10-145-129A-395
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-09-984-834-1 US-09-984-834-1 US-09-864-761-33582 US-09-797-543-5 US-09-797-543-5 US-09-797-543-5 US-09-794-975-4 US-09-155-076-14 US-09-155-4 US-09-153-4 US-09-895-443-2 US-09-895-443-2 US-09-895-443-2 US-09-895-443-2 US-09-895-443-2 US-09-895-443-2 US-09-895-443-2 US-09-895-443-2 US-09-794-975-13 US-09-794-975-13 US-09-794-975-13 US-09-794-975-13

Sequence Sequence

US-09-794-743-12 US-09-795-847-14

ALIGNMENTS

US-09-794-927-14 US-09-795-847-10 US-09-795-847-12

33582, A 34163, A 5, Appli

Appli Appli

Sequence

Appli

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       November 9, 2002, 14:03:09; Search time 6.15385 Seconds (without alignments) 23.430 Million cell updates/sec
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/cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/NSO6_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO1_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO1_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO1_PUBCOMB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*
5.1.3
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92612 seqs, 14418503 residues
   GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
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                                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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57
1 CVGSNKGAIC 10
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Match Length DB
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                                                                                                                  OM protein
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Gaps
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US-09-866-898-4

Sequence 4, Application US/09866898

Sequence 4, Application US/09866898

Sequence 4, Application US/09866898

Sequence 4, Application US/09866898

Sex Applicant NUS/0200519881

APPLICANT: Glchrest, Barbara A.

APPLICANT: Yaar, Mina

TITLE OF INVENTION: MILHENDS FOR DIAGNOSING AND TREATING

TITLE OF INVENTION: ALZHEIMER'S DISEASE

FILE REFERENCE: BU96-09A2

CURRENT APPLICATION NUMBER: US/09/866,898

CURRENT FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1996-03-29

PRIOR FILING DATE: 1996-03-29

NUMBER OF SEQ ID NOS: 5

SSOFTWARE: PastSEQ for Windows Version 3.0

LENGTH: 10
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100.0%; Pred. No. 0.00013;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Cyclic peptide US-09-866-898-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 10; Conservative
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US-09-771-161A-171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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Sequence 1, Appli
Sequence 16, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 1, Appli
Sequence 3, Appli
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Sequence

US-09-866 898-4 US-09-771-161A-171 US-09-866 898-1 US-09-972-475-16 US-09-972-475-16 US-09-87-847-2 US-09-87-847-2 US-09-89-815-1 US-09-89-815-1 US-09-89-815-1 US-09-80-815-1 US-09-80-815-1 US-09-80-815-1 US-09-80-80-1 US-09-80-80-1 US-09-80-80-1 US-09-80-80-1 US-09-972-475-1 US-09-972-475-1

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TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09972475 Patent No. US20020098173A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DeConti, Giulio A.
                                                                                                                                                                                                                                                                                                                                                                                     68.4%; Scor
100.0%; Pro
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.vv
                                                                                                                                                                 NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 35
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Patent No. US2002004335A1

GENERAL INFORMATION.

APPLICANT: Chalifour, Robert

APPLICANT: Hebert, Lise

APPLICANT: Kong, Xianqi

APPLICANT: Gervais, Francine

TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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TITLE OF INVENTION: ALZHEIMER'S DISEASE
FILE REFERENCE: BU96-09A2
CURRENT APPLICATION NUMBER: US/09/866,898
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1997-03-28
PRIOR FILING DATE: 1997-03-28
PRIOR PLICATION NUMBER: 08/625,765
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.4%; Score 39; DB 10; Length 8; 100.0%; Pred. No. 7.7e+04;
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            TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFRENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 195/76
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTIN VERSION 3.0
SEC ID NO 171
LENGTH: 123
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Pred. No. 0.46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Patent No. US20020051988A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                              75.4%;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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  APPLICANT: LEVINE, et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-771-161A-171
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: All D peptides; OTHER INFORMATION: or peptidomimetics
US-09-867-847-3
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APPLICATION NUMBER: US/09/972,475
FILING DATE: QUACCY-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/17,267
FILING DATE: QUANCOWN-APPLICATION NUMBER: US/08/17,267
FILING DATE: QY-JUN-1995
ATTORNEY/AGENT NUMBER: US/07-1995
ATTORNEY/AGENT NUMBER: US/07-1995
ATTORNEY/AGENT NUMBER: US/07-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 10; Length 35;
Pred. No. 0.67;
0; Mismatches 0; Indels
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TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
FILE REFERENCE: 14445-501 CIP
CURRENT APPLICATION NUMBER: US/09/867,847
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/168,594
PRIOR FILING DATE: 1999-111-29
PRIOR PLICATION NUMBER: 09/724,842
PRIOR FILING DATE: 2000-11-28
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APPLICANT: Kong, Xiangi
APPLICANT: Kong, Xiangi
APPLICANT: Gervais, Francine
TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
TITLE OF INVENTION: AND ANYLOID RELATED DISEASES
FILE REFERENCE: 14445-501 CIP
CURRENT APPLICATION NUMBER: US/09/867,847
CURRENT FILING DATE: 2001-09-20
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/724,842
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: All D peptides; OTHER INFORMATION: or peptidomimetics
US-09-867-847-2
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APPLICANT: JODANSSON, Jan
TITLE OF INVENTION:
FILE REFERENCE: 12125-00201
CURRENT APPLICATION OF AMYLOID FORMATION
FILE REFERENCE: 12125-002001
CURRENT APPLICATION NUMBER: US/09/988,842
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US 60/251,662
PRIOR APPLICATION NUMBER: US 60/252,695
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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                                            DB 10; Length 35; 0.67;
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                                                                                         0;
                                            68.4%; Score 39; DB 100.0%; Pred. No. 0.6 iive 0; Mismatches
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Patent No. US20020143105A1
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Patent No. US20020094335A1
GENERAL INFORMATION:
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                     Query Match
Best Local Similarity lu...
8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-972-475-16
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US-09-867-847-2
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LENGTH: 40
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LENGTH: 40
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Patent No. US20020162129A1
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: LANNEELT, Lars
TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: LANNEELT-1A
CURRENT APPLICATION NUMBER: US/09/899,815
CURRENT PILLING DATE: 2001-07-09
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Sequence 2. Application US/08923055
Patent No. US20010016327A1
GENERAL INFORMATION:
APPLICANT: Dana Giulian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
68.4%; Score 39; DB 10; Length 40; 100.0%; Pred. No. 0.76; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/923,055
FILING DATE: Sept-03-97
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: & No. US20010016327Alris LLP REBET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOT Y. Beardell
REGISTRATION NUMBER: 34, 293
REFERENCE/DOCKET NUMBER: BYLR-0038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.4
Best Local Similarity 100.
Matches 8; Conservative
  Query Match 68.4
Best Local Similarity 100.
Matches 8; Conservative
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24 VGSNKGAI 31
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US-09-899-815-1
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US-08-923-055-2
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Patent No. US20020119926A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION UNMER: US/09/956,625

CURRENT APPLICATION NUMBER: US/09/956,625

CURRENT APPLICATION NUMBER: 60/233,482

PRIOR FILING DATE: 2000-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.4%; Score 39; DB 9; Length 42; 100.0%; Pred. No. 0.8; Live 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/217,098 PRIOR FLILNG DATE: 2000-07-10 PRIOR APPLICATION NUMBER: EP 00202387.7 PRIOR FILING DATE: 2000-07-07 NUMBER OF SEQ ID NOS: 4 SOFFWARE: Patentin version 3.1 SEQ ID NO 1
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Patent No. US2002009433BA1
GENERAL INFORMATION:
APPLICANT: Chalifour, Robert
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Best Local Similarity 100.vv
These 8; Conservative
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Best Local Similarity 100.00.
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-899-815-1
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US-09-956-625-26
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US-09-867-847-1
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                                                                                                                                                                                                                                                               LENGTH: 42
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FILE REFERENCE: CHOJURER-04302
CURRENT APPLICATION NUMBER: US/09/731,460
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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ACID ESTERS, PHARMACEUTICAL COMPOSITIONS
COMPRISING SAME, AND METHODS FOR INHIBITING
-AMYLOID PEPTIDE RELEASE AND/OR ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-731-460-1
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                                                                                                                                 Query Match 68.4%; Score 39; DB 10; Length 42; Best Local Similarity 100.0%; Pred. No. 0.8; Matches 8; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JEFFREY S. NISSEN
WARREN J. PORTER
EUGENE D. THORSETT
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09731460; Patent No. US20020137112A1; GENERAL INFORMATION; APPLICANT: Chojkier, Mario APPLICANT: Buck, Martina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09280966
Patent No. US20010020097A1
GENERAL INFORMATION:
APPLICANT: JAMES E. AUDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEVERLY K. FOLMER VARGHESE JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JING WD
                                        TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-625-26
                                                                                                                                                                                                                                                         24 VGSNKGAI 31
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US-09-731-460-1
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US-09-280-966-1
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SEQ ID NO 26
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NERROLOGICAL DISEASES AND DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.4%; Score 39; DB 10; Length 43; Best Local Similarity 100.0%; Pred. No. 0.82; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                               FILE REFERENCE: SOLOMON=2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-0-03
NUMBER: OF SEQ ID NOS: 33
SOUTHARE: PatentIn version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 9, 2002, 14:11:55 Job time: 7.15385 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
COTHER INFORMATION: synthetic peptide
US-09-808-037-3
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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Sequence 1. Deplication US/09904987

GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepath
TITLE OF INVENTION: Protein Assembly or Aggregation
FILE REFERENCE: 42108/26146

CURRENT APPLICATION NUMBER: US/09/904,987

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
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68.4%; Score 39; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 8; Conservative 0; Mismatches 0; Indels
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                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4
DATABASE ENTRY DATE: 2000-09-15
RELEVANT RESIDUES: (672)..(714)
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
                                                                   APPLICATION NUMBER: US/09/280,966
FILING DATE: 30-Mar-1999
CLASSIFICATION: <UNKNOWN>
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,191
FILING DATE: 21 NOV 1997
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 NOV 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-280-966-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-808-037-3
; Sequence 3, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 43 amino acids
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-622-230
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches 8; Conservative
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US-09-904-987-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              November 9, 2002, 13:59:04; Search time 26.5385 Seconds (without alignments) 77.641 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                         671580
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
                                                                                      OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1 CATDIKGAEC 10
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Perfect score:
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| S | Description | O9n7i5 leishmania | 091837 laticanda s | O8ta62 methanosarc | Ogekri homo sanien | 025253 1001119 000 | OBSSOS EXCELLES CAP | Ogazas contraction norw | 1703 CONTRACTOR OF THE STATE OF | Ogi847 laticanda s | Ogi846 laticanda e | Ogi845 laticanda s | Ogi844 laticanda s | Ogi843 laticanda s | Ogi842 laticanda s | | |
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| SUMMARIES | QI | 09N7I5 | 091837 | Q8TQ62 | 096KR1 | 025253 | 088805 | 090205 | 090076 | 091847 | 091846 | 091845 | Q91844 | Q91843 | 091842 | 091848 | 08111117 |
| | DB | 5 | 13 | 17 | 4 | S | 2 | 11 | 11 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 |
| | Query
Match Length DB | 96 | 145 | 385 | 1057 | 2653 | 189 | 351 | 512 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 154 |
| dР | Query | 71.9 | 68.4 | 66.7 | 66.7 | 66.7 | 63.2 | 63.2 | 63.2 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 |
| | Score | 41 | 39 | 38 | 38 | 38 | 36 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 32 | 35 | 35 |
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| 13 Q8UUIO
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ALIGNMENTS

| RES
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ID | RESULT 1
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ID Q9N715 | PRELIMINARY; | PRT; | 96 AA. | | | |
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| 222 | 01-0CT-2000
01-0CT-2000 | (TrEMBLrel. 15, | | ence upd | ate) | | |
| 1 E | Probable pro | <pre>prosbeta3 protein (Fragment).</pre> | Last annotation update)
(Fragment). | ration u | pdate) | • | |
| S G | LM28.233.
Leishmania maior | ion | | | | | |
| 888 | Eukaryota; E | major.
Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania. | toplastida | ; Trypan | osomatidae; | Leishmania. | |
| RN | NCB1_TAXID=3004; | 664; | | | | | |
| RP
C | SEQUENCE FROM N.A. | M N.A. | | | | | |
| R & | Murphy L., Quail M. | | D. Rajan | dream M | Harris D. Rajandream M. Iwens A | Barrell D . | |
| RL | Submitted (JUL-2000) | UL-2000) to the | to the EMBL/GenBank/DDBJ | ank/DDBJ | databases. | | |
| DR | EMBL; AL3909 | 00 | | | | | |
| 7 G | HSSP; P25451; IRYP. | HSSP; P25451; IRYP.
Interbro: IDB001253: Brotemo suctors | 4 | | | | |
| DR. | Pfam; PF0022 | Pfam; PF00227; proteasome; | e_procease
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| FΤ | | | | | | | |
| SO | SEQUENCE 9 | 96 AA; 10774 MW; | | E9E76B074C9AE991 CRC64; | 1 CRC64; | | |
| О | Query Match
Best Local Similarity | 71.98; | Score 41; | | Length 96; | | |
| Σ | Matches 7; (| vat | 1; Mismatches | tches | 2; Indels | 0; Gaps | |
| δy | 1 CATDIKGAEC | AEC 10 | | | | | |
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| A F | Q91837; | 091837; | | | | | |
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"Comparative analysis of invaded sequences from group I phospholipase A2 genes revealed some evidences about the divergence of the gene revealed some evidences about the divergence of the gene groups and families."
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A803715; BAA99510.1; -
EMBL, A8037218; BAA99510.1; -
EMBL, A8037319; BAB7246.1; -
EMBL, A806439; BAB7246.1; -
InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                                                                            Tamiya T., Fujimi T.J.;
"Laticauda semifasciata phospholipase A2 gene clone LsPLA2GL2-1 2-4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                Tamiya T., Fujimi T.J.; "Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPm09."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
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MEDLINE-21929760; PubMed-11932238;
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
                                                                                      Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.4%; Score 39; DB 13; Length 145; 60.0%; Pred. No. 4.1; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 28 145 POTENTIAL.
SEQUENCE 145 AA; 16099 MW; A6245F7C0D0ED38F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                        Phospholipase A2 precursor (EC 3.1.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00119; PA2_ASP; 1. PROSITE; PS00118; PA2_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00085; PA2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |:| |:|
116 CACDLKAAKC 125
                                                                                                                                                                                                                                                                  TISSUE-VENOM GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATDIKGAEC 10
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                NCBI_TaxID=8631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8TQ62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MA1690
                                                                                                                 snake).
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FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Yee W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Li W., Liu J., Mukhopadhyap B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Firtchett M., Sowers K.R., Jung H., Macario A.J.L., Paulsen I., Metcalf W.W., Birren B.; Metcalf W.W., Birren B.; Metcalf W.W., Allender S.H., Lander E., Metcalf W.W., Sirrell M.W., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Allender B., Allende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Kleines M., Gaertner A., Ritter K., Schaade L.;
"Cloning and expression of the human single copy homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.7%; Score 38; DB 4; Length 1057; Best Local Similarity 77.8%; Pred. No. 46; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 38; DB 17; Length 385; 77.8%; Pred. No. 17; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115287 MW; F7F6C77814146691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AA; 43984 MW; 06C276326ECEF391 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19, Last sequence update)
20, Last annotation update)
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Gene 275:157-162(2001).

BEMEL; A314799; CAC40818.1; -.

Interpro; IRP000822; Znf_C2H2.

PROSITE; PS00028; zl-C2H2; 3.

PROSITE; PS00028; Zinc-FINGER_C2H2_1; UNKNOWN_3.

BNA-Dinding; Zinc-finger.

SEQUENCE 1057 AA; 115287 MW; F7F6C77814146691
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01-DEC-2001 (TrEMBLrel. 19, Last seqt
01-MAR-2002 (TrEMBLrel. 20, Last and
Putative zinc finger protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AE010842; AAM05097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 77.8
Matches 7; Conservative
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Query Match
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0
                                             STRAIN=SS SEEKING;
MEDLYNE=5400228; PubMed=8807304;
MEDLYNE=5400228; PubMed=8807304;
MCKenzie A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., Yen J.L.,
MCKenzie J.A., Batterham P.;
"Scalloped wings is the Lucilia cuprina Notch homologue and a
candidate for the modifier of fitness and asymmetry of diazinon
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
NCBL_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 38; DB 5; Length 2653; 60.0%; Pred. No. 1.1e+02; 7ative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
40S ribosomal protein S3A (Lysin-rich KRP-A) (S1 in yeast).
ECU05_0250.
                                                                                                                                                                                            STRAIN-SS SEEKING;
Chen Z., McKenzie J.A., Batterham P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF023672; AAC36152.1;
EMBL, AF032672; AAC36152.1;
EMBL, AF032671; AAC36152.1;
EMBL, AF032671; AAC36152.1;
EMBL, AF032673; AAC36152.1;
EMBL, AF032673; AAC36152.1;
EMBL, AF032673;
AAC36153.1;
                                                                                                                                                         Chen Z., Newsome T., McKenzie J.A., Batterham P.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285928 MW; 6AF2A058FEEC6329 CRC64;
                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                     Frant, PF00023; ank; 6.
Pfam; PF00068; EGF; 36.
Pfam; PF00066; notch; 3.
PKINTS; PR00101; EGFBLCOD.
PRINTS; PR01452; NOTCH.
SMART; SM00179; EGF_CA; 4.
SMART; SM00179; EGF_CA; 24.
SMART; SM00001; EGF_1ike; 11.
                                                                                                                   Genetics 143:1321-1337(1996).
                                                                                                                                      SEQUENCE OF 39-265 FROM N.A. STRAIN-SS SEEKING;
                                                                                                                                                                                       SEQUENCE OF 39-265 FROM N.A.
                                                                                                                                                                                                                                                                                                                  InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR000800; Notch.
                                                                                                                                                                                                                                                                                      InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydroxylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2653 AA;
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418 CATGYKGVDC 427
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                                    SEQUENCE FROM N.A.
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Q8SS05;
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TO SEQUENCE FROM N. A.

SEQUENCE FROM N. A.

SEQUENCE FROM N. A.

STAIN-SPRAGUE-DAWLEY;

WEDLINE-20035752; PubMed=10570975;

Liu C., Liu X.J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,

Liu C., Liu X.J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,

Liu C., Liu X.J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,

Liu C., Liu X.J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,

R. Ling N., De Souza E.B., Maki R.A.;

That Induces protein tyrosine phosphorylation.";

K. Gene 238471-478(1999).

R. Matter Prof. 1PR000359; Cys. Knot.

R. InterProf. 1PR000359; Cys. Knot.

R. InterProf. 1PR000864; TSP1.

R. InterProf. 1PR000967; INSI. Grower C.

R. InterProf. 1PR000967; UWF.C.

R. InterProf. 1PR00099; VWF.C.

R. Pfam, PF000091; VWF.C.

R. Pfam, PF00099; VWC: 1.

R. Pfam, PF00099; VWC: 1.
                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 36; DB 5; Length 189; 85.7%; Pred. No. 22;
Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBL_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                          Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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SWART; SW00121; IB; 1.
SWART; SW00210; TSP1, 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; GTCK_2; 1.
PROSITE; PS01208; VWFC; UNKNOWN_1.
SEQUENCE 351 AA; 38509 MW; 02619707DE7C1BFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 85.7 es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                          SEQUENCE FROM N.A.
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42 DIKGSEC 48
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                                                                                                                                   STRAIN=GB-M1;
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DB 11; Length 351;

63.2%; Score 36;

145 AA

PRT;

PRELIMINARY;

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Query Match
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SIGNAL
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                                                                                                                                                                                                                              snake).
                          091847;
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HD DATE OF THE PET OF 
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X MEDLINE-21085660; PubMed=1121851;

X Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Shinagawa A., Shibata K., Xonno H., Adachi J., Fukuda S.,

A Arawa W., Izawa M., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,

A Alawa K., Izawa M., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,

R Alato T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,

R Radota K., Matsuda H.A., Ashburner M., Bertalov S., Casavant T.,

R Radota K., Matsuda H.A., Ashburner M., Bertalov S., Casavant T.,

R Radota K., Matsuda H.A., Ashburner M., Bertalov S., Casavant T.,

R Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

R Sakai K., Okido T., Furnon M., Aono H., Baldarelli R., Barsh G.,

R Brownstein M.J., Bult C., Fletcher C., Fulita M., Garibodi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

R Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Alayashizaki R., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

R Alayashizaki Y.,

R Hayashizaki W.,

R Hayashizaki Y.,

R Hayashizaki W.,

R Hayashizaki 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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IN ALUTE 409:68-690 (2001).

R EMBL, AROLTY80: BAB30928.1: -.

R EMBL, AROLTY80: BAB30929.1: -.

R MGD, MGI.1913900; 5730521E12Rik.

R INTEPTO: IPRO00483: LRR.Cterm.

IN INTEPTO: IPRO00483: LRR.Cterm.

R INTERPO: IPRO00372; LRR.Nterm.

R INTERPO: IPRO00591 LRR.Lyp.

R INTERPO: IPRO00591 LRR.Lyp.

R Pfam; PF00463; LRR.Lyp.

R Pfam; PF00463; LRR.Lyp.

R Pfam; PR001463; LRR.Typ.

R Pfam; PR001463; LRR.Typ.

R PAINTS; PR00019; LENRI; 1.

R SMART; SM00019; LENRI; 1.

R SMART; SM00013; LRR.Typ.

R SMART; SM000146; LRR.Typ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                             Indels
                                                                                                                                                                                                                                                                                                          09C076;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                             7;
                                                                                                                                                                                                                                                                                         512 AA
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  66.7%; Pred. No. 40; ive 2; Mismatches
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                   6; Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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     Best Local Similarity
Matches 6; Conserv
                                                                                                                      111:11 :1
250 ATDMKGKKC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                     2 ATDIKGAEC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5730521E12RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                   RESULT 8
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CA1847
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Tamiya T., Fujimi T.J.;
"Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cL038.";
"Laticauda semifasciata phospholipase A2 cDNA clone GNBLA2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037410; BAB03297.1;
HSSP; P00608; LAE7.
                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-VENOM GLAND;
Tamiya T., Fujimi T.J.;
Tamiya T., Fujimi T.J.;
"Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cL037.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037409; BAB03296.1; -.
HSSP; P00608; 1AE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
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                                                                                                                                                 Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
D3BC01790A0F7885 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2.; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_ASP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPRO01211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
PRODOM; PD000303; PHPHLIPASEA2.
SMART; SM00085; PAA2.
PROSITE; PS00119; PAA2.ASP; 1.
PROSITE; PS00119; PA2.ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL 1 27 P
SEQUENCE 145 AA; 16062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phospholipase A2 precursor.
                                                                                                 Phospholipase A2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.C
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
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TISSUE=VENOM GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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us-09-632-748-9.rspt

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Query Match
Best Local Similarity
5; Conserva
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116 CACDLQAAKC 125
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TISSUE=VENOM GLAND;
                                                                                                                                                                                                           1 CATDIKGAEC 10
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                                                                                                                                                                 Query Match
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SIGNAL
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                                                                                                                                                                                                                                                                                             Q91843;
                                                                                                                                                                                                                                                                                                                                                                        snake).
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                                                                                                                                                                                     Matches
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                                            Gaps
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TSORD-WERDM GLAND;
Tamiya T., Fulini T.J.;
"Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPt09.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037411; BBB03298.1;
HSSP; P00608; IAE7.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                     61.4%; Score 35; DB 13; Length 145; 50.0%; Pred. No. 27; 27; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 35; DB 13; Length 145; 50.0%; Pred. No. 27; tive 3; Mismatches 2; Indels
                                           2; Indels
145 AA; 16059 MW; 9277AC82B50F7887 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9277B0F2BC7F6D87 CRC64;
                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Phospholipase A2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phospholipase A2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                 InterProj IPR001211; PhospholipaseA2.
Pfam. PF00068; phoslip; 1.
PRIMES. PR00389; PHPHILPASEA2.
PRODOM; PD000303; PhospholipaseA2; 1.
SMART; SMORDS; PA22, 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL 1 27 P
SEQUENCE 145 AA; 16089 MW;
          Ouery Match
Best Local Similarity 50.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tamiya T., Fujimi T.J.;
                                                                           || |:: |:|
|16 CACDLQAAKC 125
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|16 CACDLQAAKC 125
                                                             1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CATDIKGAEC 10
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SEQUENCE
                                                                                                                                      Q91845
Q91845;
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Q91844;
                                                                                                                                                                                                                           snake).
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Q91845
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Q91844
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Gaps
"Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPt10.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037412; BAB03299.1;
HSSP; P00608; IAE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tamiya T., Fujimi T.J.;
"Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPm05.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB037413; BAB03300.1; -.
HSSP; P00608; 1AE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                    61.4%; Score 35; DB 13; Length 145; 50.0%; Pred. No. 27; 1.1ve 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                   SIĞNAL 1 27 POTENTIAL.
SEQUENCE 145 AA; 16073 MW; 49D4B439160F7895 CRC64;
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SEQUENCE 145 AA; 16073 MW; 926F0F88861DE887 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Phospholipase A2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                       Interpro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SW00085; PA2.; 1.
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_AS; 1.
PROSITE; PS00118; PA2_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 50.0
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Fujimi T.J., Tsuchiya T., Tamiya T.;

Fujimi T.J., Tsuchiya T., Tamiya T.;

Fujimi T.J., Tsuchiya T., Tamiya T.;

Comparative analysis of invaded sequences from group I phospholipase
A2 genes revealed some evidences about the divergence of the gene
groups and families.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB062440; BAB72247.1; -.

HSSP; P00608; 1AB7

InterPro; PRR01211; PhospholipaseA2.

PFRUNT; PR00089; phoslip; 1.

PRINTS; PR00389; PhospholipaseA2;

ProDom; P000033; PhospholipaseA2; 1.

SMART; SM00085; PA2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taboura various attended to the EMBL/GenBank/DDBJ databases.
Taticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPm08.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB031414; BAB0310.1;
HSSP; P00608; IAE7.
HTAEPPP. TRR001211; PhospholipaseA2.
Pfam; PF00068; phos11p; 1.
PRINTS; PR00088; PHPHLIPASEA2.
SMART; SM00085; PA2c; 1.
PROSTITE; PS00118; PA2_ASP; 1.
PROSTITE; PS00118; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                          Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 35; DB 13; Length 145; 50.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
1F84DF6F7BC5348F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6626FDC7AE0ED39D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNV-2002 (TrEMBLrel. 21, Last annotation update)
Phospholipase A2 precursor (EC 3.1.1.4).
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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SEQUENCE 145 AA; 15900 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL 1 27 P
SEQUENCE 145 AA; 16085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00119; PA2_ASP; 1. PROSITE; PS00118; PA2_HIS; 1.
                                             Phospholipase A2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.۰۰
در 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 CACDLQAAKC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Hydrolase. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=VENOM GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
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Q91848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE SET THE PROPERTY OF THE PR
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Ouery Match
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CATDIKGABC 10
I | |: |: |
Db 116 CACDIEAAKC 125
Search completed: November 9, 2002, 14:03:02
Job time : 28.5385 secs
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 9, 2002, 13:57:44; Search time 7.69231 Seconds (without alignments) 53.919 Million cell updates/sec Run on:

US-09-632-748-9 57 1 CATDIKGAEC 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | Description | O9ndal trypanosoma | | | _ | - | | P00612 laticauda s | P00613 laticauda s | | | P17980 homo sapien | | | bos t | Q29074 sus scrofa | pos | xeno | | | mus m | | P05200 gallus gall | | P30363 bacillus li | Q9hvj9 pseudomonas | Q02833 homo sapien | 054803 mus musculu | P51579 rattus norv | homo |) ношо | уошо | 08 halob | P00080 rhodopila q |
|-----------|--------|-------------|--------------------|------------|------------|------------|------------|------------|--------------------|--------------------|------------|------------|--------------------|----------|------------|------------|-------------------|-----------|-----------|-----------|-----------|-----------|---------|--------------------|---------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|------------|------------|----------|--------------------|
| SUMMAKIES | | DI CI | PSB3_TRYBB | MOM2_CAEEL | UBP4_HUMAN | TAC2_MOUSE | NOTC_DROME | PA21_LATSE | PA23_LATSE | PA24_LATSE | PA21_OXYSC | PRSB_XENLA | PRSA_HUMAN | PRSA_RAT | TIE2_HUMAN | TIEZ_BOVIN | NGF_PIG | NGF_BOVIN | NGF_XENLA | NGF_CAVPO | NGF_HUMAN | NGF_MOUSE | NGF_RAT | NGF_CHICK | PSA7_YEAST | ASPG_BACLI | RTCA_PSEAE | CK13_HUMAN | P2X6_MOUSE | P2X6_RAT | UD13_HUMAN | UD14_HUMAN | UD15_HUMAN | 5 | CY2_RHOGL |
| | | DB : | 1 | ٦ | Н | ~ | Н | Н | Н | H | Н | - | | ~ | Н | Н | ~ | ~ | Н | Н. | П | П | П | - | . | | - | - | - | - | - | Η, | Н, | ٠, | - |
| | | Length | 205 | 362 | 963 | 1035 | 2703 | 118 | 118 | 118 | 119 | 404 | 439 | 439 | 1124 | 1125 | 229 | 231 | 231 | 241 | 241 | 241 | 241 | 243 | 254 | 322 | 341 | 373 | 379 | 379 | 534 | 534 | 534 | 81 | 106 |
| æ | Query | Match | 71.9 | 2.99 | 66.7 | 66.7 | 2.99 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | | | 29.6 | | 29.6 | | | | | | | | | | | | | | 57.9 | |
| | | Score | 41 | 38 | 38 | 38 | 38 | 35 | 35 | 35 | 35 | 32 | 32 | 32 | 3 | 32 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | | | en c | |
| | Result | No. | П | 7 | ო | 4 | Ŋ | 9 | 7 | Φ. | σ, | 70 | . | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 13 | 20 | 21 | 22 | 573 | 77 | 522 | 97 | 77 | 58 | 57.0 | 30 | 4.
1.0 | 2 0 | 3,5 |

1 CATDIKGAEC 10

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| P54021 methanococc Q57793 methanococc Q46948 escherichia P55880 salmonella O74175 schizosacch P20675 praomys nat Q9thi helicobacte Q95171 callithrix Q92731 homo sapien P35123 mus musculu |
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
- FRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEEN INVOLVED
IN ENDODERM SPECIFICATION AND CLEAVAGE AXIS DETERMINATION.
-!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                STRAIN-Bristol N2;
MEDILINE-97433081; PubMed-9288750;
REDILINE-97433081; PubMed-9288750;
ALI M., Priess J.R., Mello C.C.;
"Wht signaling and an APC-related gene specify endoderm in early C. cell 90:707-716(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOM-2 PROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
ED69435F1F4F40DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 362;
Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                            Gattung S., Le T.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                      MOM2_CAEEL STANDARD; PRT; 362 AA. 010459; 016146; 16-0cr-2001 (Rel. 40, Created) 16-0cr-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBE, U41996; AAA83472.2; ...
Wormbep; FSBE1.7; CE17806.
InterPro; IPR000970; Wnt_grthfactor.
Pfam; PF00110; Wnt; 1.
SMART; SMO097; WnT1; 1.
Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF013952; AAC47749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AA; 40190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                       extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                          Mom-2 protein precursor.
MOM-2 OR F38E1.7.
                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 CAIDVKDREC 313
122 CATDLIGAPC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                  [3]
REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                            MOM2_CAEEL
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                                 RESULT 2
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RESULT 3

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SSGVSRG -> N (IN ISOFORM UNPES).
C->A: LOSS OF ACTIVITY.
S -> R (IN REF. 3).
R -> S (IN REF. 3).
W; 1B62B752F9410CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=98124180; Pubmed=946453;
Frederick A., Rolfe M., Chiu M.I.;
The human UNP locus at 3p21.31 encodes two tissue-selective,
cytoplasmic isoforms with deubiquitinating activity that have reduced
expression in small cell lung carcinoma cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family; Proto-oncogene; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Prain cortex;

BEDLINE=95303480; bubmed=7784062; Gray D.A., Inaxawa J., Gupta K., Wong A., Ueda R., Takahashi T.;

"Elevated expression of Unph, a proto-oncogene at 3p21.3, in human
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                    thiolesterase 4) (Ubiquitin specific processing protease 4) (Deubiquitinating enzyme 4) (Ubiquitous nuclear protein homolog). USP4 OR UNP OR UNPH.
UBP4_HUMAN STANDARD; PRT; 963 AA.
Q13107; 043453;
Q13107; 043453;
O1-NOV-1997 (Rel. 35, Created)
15-UUL-1998 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15) (Ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray D.A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF017305; AAC27355.1; -. EMBL; AF017306; AAC27356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00972; UCH_2_1; 1.
PROSITE; PS00973; UCH_2_2; 1.
PROSITE; PS50235; UCH_2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U20657; AAB72237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001394; UCH-2.
Pfam; PF00442; UCH-1; 1.
Pfam; PF00443; UCH-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 10:2179-2183(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C19.010; -.
Genew; HGNC:12627; USP4.
                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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CONFLICT
SEQUENCE
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VARSPLIC
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                                                                                                                                                                                                                                                    Gaps
                     Gaps
                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                    ;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%; Score 38; DB 1; Length 1035;
 DB 1; Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-LYS.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
WW. 0698015282F94C78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                    Indels
                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transforming acidic colled-coll-containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTC_DROME STANDARD; PRT; 2703 AA. P07207; P04154; 097458; 09W4T8; 10.1NOV-1986 (Rel. 03, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Neurogenic locus Notch protein precursor. No Res:140611.1 OR EG:163A10.2 OR CG3936.
                                                                                                         PRT; 1035 AA.
                                                                                                                                                                                                                                                                                                                                SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TACC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 13;
66.7%; Score 38; 50.0%; Pred. No.
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834 1034 COII
1035 AA; 112715 MW;
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                    Conservative
                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02649; 1LE4.
MGD; MGI:1928899; Tacc2
                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 CSADSKGQEC 143
                                                  |:| : |:||
568 CSTSVDGSEC 577
                                       1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATDIKGAEC 10
           Best Local Similarity
                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                          TAC2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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  Query Match
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                                                                                               TAC2_MOUSE
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On Croscopila methorogaster (Fittle filt).

Charactor, Retargot; Norpeters; Endopetsygots Dippersa Brachycers;

On Insects; Persygots; Norpeters; Endopetsygots Dippersa Brachycers;

ON NORTHITAKING-127;

NORTHITAKING-128;

NORTHITAKING-128;
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Harris W.A.;

**Harris W.A.;

**Harris W.A.;

**T "Many cell types specified by Notch function.";

**L Curr. Biol. 1:120-122(1991).

**L Curr. Biol. 1:120-122(1991).

**C -!- FUNCTION: Functions as a receptor for membrane-bound ligand belta and Serrate to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with Su(H)

**Suppressor of hairless) and activates genes of the enhancer of Suppressor of hairless) and activates genes of the enhancer of Split locus. Essential for proper differentiation of ectoderm.

**C -:- SUBLIARITY: BELONGS TO THE NOTCH FAMILY.**

**C -:- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.**

**C -:- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.**

**C -:- SIMILARITY: CONTAINS 6 ANK REPEATS.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                SEQUENCE OF 2505-2611 FROM N.A.
MEDILINE-68099329; Pubmed-2981631;
Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
"Opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in D. melanogaster.";
                                                                                                                                                                                                                                                                                                 FEGURENCE OF 1-8 FROM N.A.
MEDLINE=87257846; PubMed=3037327;
Kelley M.R., Kidd S., Berg R.L., Young M.W.;
"Restriction of P-element insertions at the Notch locus of Drosophila
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Millian P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                             "From sequence to chromosome: the tip of the x chromosome of D. melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                Mol. Cell. Biol. 7:1545-1548(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; K03508; AAA26725.1; --
EMBL; M1369; AAA28725.1; --
EMBL; K03507; AAA28725.1; JOINED.
EMBL; AE004426; AAF45848.2; --
EMBL; AL035436; CAB37610.1; JOINED.
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF_11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000742; EGE_2.
InterPro; IPR001881; EGE_Ca.
InterPro; IPR001438; EGE_II.
InterPro; IPR002049; LaminIn_EGF.
InterPro; IPR000800; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M12175; AAA74496.1; -. EMBL; M16025; AAA28726.1; -.
                                                                                                                              Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A05267; A05267.
HSSP; P00740; IEDM.
FlyBase; FBgn0004647; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A24420; A24420.
PIR; A24768; A24768.
                                                                                                                                                                                                                                                                   Cell 40:55-62(1985).
                                                                             Glover D.M.;
                                                                                                                                                                                                                                                                                                                                                                                  melanogaster
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EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 22.
EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 23.
                                                                                                                                                                                                                                                                                                                                                                                                                        CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                         EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 8.
EGF-LIKE 8.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                             Receptor; Transcription regulation; Activator; Differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-acylhydrolase).
Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
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Elapidae; Laticaudinae; Laticauda.
NCBI_TaxID=8631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 isozyme I (EC 3.1.1.4) (Phosphatidylcholine
                                                                                                                                                                                                                                             NEUROGENIC LOCUS NOTCH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 2703;
                                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM-BINDING
                                                                                                                                                                                                       Developmental protein; Neurogenesis; Repeat; ANK repeat;
EGF-like domain; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                    SMART; SMO0248; ANK; 7.

SMART; SMO0181; EGF; 36.

SMART; SMO019; EGF_CA; 35.

SMART; SMO0004; NL; 2.

PROSITE; PS50088; ANK_REPEAT; 5.

PROSITE; PS50207; ANK_REP_REGION; 1.

PROSITE; PS00002; EGF_1; 34.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01187; EGF_CA; 21.
                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                 POTENTIAL
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Pfam; PF00008; EGF; 36.
Pfam; PF00023; ank; 6.
Pfam; PF00066; notch; 3.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.78;
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les 6; Conservative
                                                                                                                                                                                                                                           437 CATGYKGVDC 446
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DOMAIN
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NCBI_TaxID=8631;
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         TISSUE=Venom;
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P00613;
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CA_BIND
SEQUENCE
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HIGH SPECIFIC ACTIVITY REDUCED 20-FOLD
BY MODIFICATION OF TRP-64.
                                                                                                                                                                                                                                                                                          BY MODIFICATION OF TRP-64.

BY SIMILARITY.

VIA CARBONYL OXYGEN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                           Nishida S., Kim H.S., Tamiya N.;
"Amino acid sequences of three phospholipases A I, III and IV from
the venom of the sea snake Laticauda semifasciata.";
Blochem. J. 207:589-594(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 isozyme III (EC 3.1.1.4) (Phosphatidylcholine 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                             MEDLINE-89044898; PubMed-3188064;
Takasaki C., Kuramochi H., Shimazu T., Tamiya N.;
"Correction of amino acid sequence of phospholipase A2 I from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                               Hydrolase; Lipid degradation; Calcium; Multigene family; Venom. ACT_SITE 48 48
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Elapidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Blapidae; Laticaudinae; Laticauda.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            F3BCC43C215B89CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             61.4%; Score 35; DB 1
50.0%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                     Interpro; IPR001211; PhospholipaseA2.
Pfam, PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
PRODOM; PD000303; PhospholipaseA2; 1.
                  MEDLINE-83153048; PubMed=7165712;
                                                                                                                                                                                                                                                                                                                                                                                                             13131 MW;
                                                                                                                                                                                                                                                PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                     REVISIONS TO 70-80.
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P00612;
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"Amino acid sequences of three phospholipases A I, III and IV from the venom of the sea snake Laticanda semifasciata.";
Biochem. J. 207:589-594(1982).
-i- FUNCTION: PA2 CAPALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
MEDINE-83153048; PubMed=7165712;
Nishida S., Kim H.S., Tamiya N.;
*Mainto acid sequences of three phospholipases A I, III and IV from the venom of the sea snake Laticauda semifasciata.";
Blochem. J. 207:589-594(1982).
-!- FUNCTION: PAZ CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-ROLYI GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
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VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.-UUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 isozyme IV (EC 3.1.1.4) (Phosphatidylcholine 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium; Multigene family; Venom.
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                                                                                                                                                                                                                                                                                                                                                                   acylglycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-!- FIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-!- FIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
-!- FIMILARITY: PROFILE TO THE PHOSPHOLIPASE A2 FAMILY.
-!- FIMILARITY: PROFILE TO THE PHOSPHOLIPASE A2.
-!- FIMILARITY: PROFILE TO THE 
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Elapidae; Laticaudinae; Laticauda.
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MEDLINE=83153048; PubMed=7165712;
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PROSTTE; PS00118; PA2_HIS; 1.
PROSTTE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; 48
ACT_SITE
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Matches 5; Conservative
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-! FUNCTION: Taipoxin is the most potent animal toxin known. The alpha chain possesses a phospholipase activity.
-! CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion.
-!-COFACTOR: Binds I calcium ion per subunit (By similarity).
-!-SUBUNIT: CONTAINS THREE NONCOVALENTLY BOUND CHAINS (ALPHA, BETA, AND GAMMA), EACH RELATED TO PHOSPHOLIPASE A2.
-!-SUBCELLULAR LOCATION: Secreted.
-!- MISCELLULAR LOCATION: Sereted.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PIR, A00754; PSOXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lind P., Eaker D.;
"Amino-acid sequence of the alpha-subunit of taipoxin, an extremely potent presynaptic neurotoxin from the Australian snake taipan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIA CARBONYL OXYGEN (BY SIMILARITY). VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxyuranus scutellatus scutellatus (Australian taipan).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae: Acanthophiinae; Oxyuranus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIA CARBONYL OXYGEN (BY SIMILARITY). VIA CARBONYL OXYGEN (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
-1- COFACTOR: Binds I calcium ion per subunit (By similarity).
-1- SUBCELLUIAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2, taipoxin alpha chain (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA.
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SIMILARITY.
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MEDLINE-82261658; PubMed-7049694;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13241 MW;
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50.0%;
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HSSP; P00608; 1AE7.
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P00614;
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CA_BIND
SEQUENCE
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                                               PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Calcium; Presynaptic neurotoxin; Venom; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
26S protease regulatory subunit 6A (TAT-binding protein 10) (TBP-10).
TBP10.
                                                                                                                        BY SIMILARITY.
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                    61.4%; Score 35; DB 1; Length 119;
                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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         InterPro: IPR001211; PhospholipaseA2.
Pfam: PF00068; phoslip: 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
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                                                                                                                                                                                                                                                                                            13829 MW;
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                                                                                                                                                                                                                                                                                                                                               6; Conservative
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HSSP; P00608; 1AE7
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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90 CRCDAKAAEC 99
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042586;
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DISULFID
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MUTAGEN
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Local Complex (BY SIMILARITY).

FUNCTION: INTERACTS WITH THE HUMAN IMMUNOBEFICIENCY VIRUS TAT TRANSACTIVATION. SPECIFICALLY SUPPRESSES TAT WEDIATED TRANSACTIVATION. PROBABLY INVOLVED IN ATP HYDROLYSIS. IT IS PROSIBLE THAT PROTEINS MSSI AND TBP-1 COMPRETE WITH EACH OTHER TO REGULARE THE INTERACTION WITH THE TRANSCRIPTIONAL COMPLEX WITH THE HIV GENE, THEREBY INFLUENCING GENE EXPRESSION IN BOTH DIRECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demartino G.N., Proske R.J., Moomaw C.R., Strong A.A., Song X., Hisamatsu H., Tanaka K., Slaughter C.A.; Hisamatsu H., Tanaka K., Slaughter C.A.; Identification, purification, and cracerization of a PA700-dependent activator of the proteasome.", J. Biol. Chem. 271:3112-318(1996).

-i- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90302011; PubMed-2194290; Nelbock P., Dillion P.J., Perkins A., Rosen C.A.; "A cDNA for a protein that interacts with the human immunodeficiency virus Tat transactivator."
                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
265 protease regulatory subunit 6A (TAT-binding protein 1) (TBP-1)
(Proteasome subunit P50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The type 1 human immunodeficiency virus Tat binding protein is a transcriptional activator belonging to an additional family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=93126329; PubMed=8419915;
Ohana B., Moore P.A., Ruben S.M., Southgate C.D., Green M.R.,
                                                                                                                                                          61.4%; Score 35; DB 1; Length 404; 50.0%; Pred. No. 21;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                192 199 ATP (POTENTIAL).
404 AA; 45276 MW; FC988BBBDCEFC2E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evolutionarily conserved genes.";
Proc. Natl. Acad. Sci. U.S.A. 90:138-142(1993).
                                                                                                                                                                                                                                                                                                                       439 AA.
                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                       Pred. No. 21;
            InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR003960; AAA_sub.
Pfam; PF000004; AAA; 1.
SMART; SM00382; AAA; 1.
TIGRPAMS; TIGR01242; 26Sp45; 1.
PROSITE; PS00674; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96216387; PubMed=8621709;
InterPro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 36-439 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 248:1650-1653(1990)
                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                               352 CTDDFNGAQC 361
                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                    1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                    Q96HD3;
                                                                                                                                                                                                                                                                                                                                                                                                                       PSMC3 OR TBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                     PRSA_HUMAN
P17980; 096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen C.A.;
                                                                                                                                SEQUENCE
                                                                                                                                                             Query Match
                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                       PRSA_HUMAN
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rivkin E., Cullinan E.B., Tres L.L., Klerszenbaum A.L.; rototein associated with the manchette during rat spermiogenesis is encoded by a gene of the TBP-1-like subfamily with highly conserved ATPsee and protease domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver;
MEDLINE=96183075; PubWed=8607789;
MAKINO Y., Yogosawa S., Kanemaki M., Yoshida T., Yamano K.,
Makino Y., Yogosawa S., Kanemaki M., Muramatsu M., Tamura T.;
Kishimor T., Moncollin V., Egly J.M., Muramatsu M., Tamura T.;
"Structures of the rat proteasomal ATPases: determination of highly conserved structural motifs and rules for their spacing.";
Biochem. Blophys. Res. Commun. 220:1049-1054(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q63569; P97638;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
26S protease regulatory subunit 6A (TAT-binding protein 1) (TBP-1)
(Spermatogenic cell/sperm-associated TAT-binding protein homolog
SUBUNIT: MAY FORM A HETERODIMER WITH A RELATED FAMILY MEMBER.
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                   -:- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (Potential).
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Pred. No. 23;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K->H: LOSS OF FUNCTION.
D->A: LOSS OF FUNCTION.
R -> A (IN REF. 1 AND 3).
OE443465DDDEBB0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IFRUGGGGG, AAA; 1.
Pfam; PF00004; AAA; 1.
TICRFAMS; TICR01242; 265p45; 1.
PROSITE; PS00674; AAA; 1.
Proteasome; ATP-binding; Nuclear protein.
227 234 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 AA.
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR003960; AAA_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley;
MEDLINE-97410049; PubMed-9266764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Reprod. Dev. 48:77-89(1997).
                                                                                                                                                                                                                                                                     EMBL; M34079; AAA36666.1; -. EMBL; BC008713; AAH08713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49203 MW;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:9549; PSMC3.
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289
409
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                                                                                                                                                                                                                                                                                                                     PIR; A34832; A34832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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289
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Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J.,
Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C.,
Mulliken J.B., Olse B.R.;
                                            THE REGULATORY (OR ATPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                          DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE 26S COMPLEX (BY SIMILARITY).
SUBUNIT: MAY FORM A HETERODIMER WITH A RELATED FAMILY MEMBER.
SUBCELLULAR LOCATION: CYLOPIASMIC and nuclear (Potential).
SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiopoietin 1 receptor precursor (EC 27.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEE) (Tyrosine-protein kinase receptor TEE) (Tyrosine-protein kinase receptor TEE) (Tunica interna endothelial cell kinase) (CD202b antigen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.4%; Score 35; DB 1; Length 439; 50.0%; Pred. No. 23; 1ve 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U77918; AAB70882.1; ALT_INIT.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR003969; AAA_ATPase.

InterPro; IPR003969; AAA_Sub.

Pfam; PF00004; AAA; 1.

SNART; SM00382; AAA; 1.

PROSITE; PS00674; AAA; 1.

Proteasome; ATP-binding; Nuclear protein.

NP_BIND 27 234 ATP.

NP_BIND 27 234 ATP.

CONFLICT 84 84 K -> N (IN REF. 2).

CONFLICT 317 317 L -> M (IN REF. 2).

SEQUENCE 439 AA; 49160 MW; 292E780AEBD19BAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D83522; BAA11939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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Matches 5; Conserv
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Q02763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PREDOMINAWILY EXPRESSED IN ENDOTHELIAL CELLS
AND THEIR PROGENITORS, THE ANGIOBLEASTS. HAS BEEN DIRECTLY FOUND
IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
ENDOTHELIAL CELLS, BRAIN AND KIDNEY.

ENDOTHELIAL CELLS, BRAIN AND KIDNEY.

BALFORMATIONS (VMCM.), AN BRROW OF VASCULAR MORPHOGENESIS
CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
                                                    Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBLABILY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
DATABASE: NAME=PROW; NOTE=PROW 3:12-14(2002);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1715848914_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE
                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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EGF-LIKE 1.
EGF-LIKE 2.
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PRODOM; PROUDOSS, TYRKINASE.
PRODOM; PROUDOSS, 1.
SMART; SMOOOSS, EGF_11ke; 1.
SMART; SMOOOSS, EGF_11ke; 1.
SMART; SMOOOSS, FORS; 3.
SMART; SMOOOSS, FORS; 3.
PROSTITE; PSOOLOS; PROTEIN_KINASE_ATP; 1.
PROSTITE; PSOOLOS; PROTEIN_KINASE_DOM; 1.
PROSTITE; PSOOLOS; PROTEIN_KINASE_DOM; 1.
PROSTITE; PSOOLOS; EGF_1; 3.
PROSTITE; PSOOLOS; EGF_1; 3.
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InterPro; IPR000191; Euk_Dkinase.
InterPro; IPR0001961; FN_III.
InterPro; IPR001245; TY_Dkinase.
Pfam; PP00008; EGF; 1.
Pfam; PF000041; fn3; 3.
Pfam; PF000641; fn3; 3.
                              MEDLINE=99299243; PubMed=10369874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L06139; AAA61139.1; -. HSSP; P11362; 1FGK.
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MIM; 600221; -.
MIM; 600195; -.
                                                                                                                                                                                                                                                                                                                                                           FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY.
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NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
NGF_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
   ŏ
                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIGURE FROM N.A.

TISSUE-Endothelial cells;

MEDLINE-94022374; Pubmed-8415706;

Sato T.N., Qin Y., Kozak C.A., Andus K.L.;

Tile-1 and tie-2 define another class of putative receptor tyrosine kinase genes expressed in early embryonic vascular system.";

Proc. Natl. Acad. Sci. U.S.A. 90:9355-9388(1993).

--- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR FOR ANGIOPOIETIN I. TY MAY CONSTITUTE THE EARLIEST MANMALIAN ENDOTHELIAL CELL INRAGE MARKER. PROBABLY REGULATES ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SÜBCELLULÂR LÖCATION: TYPE I membrane protein.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiopoletin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
                                                                                                                                                                                                       R -> W (IN VMCM1; ACTIVATING EFFECT).
/FIId-VAR_006352.
Y -> S (IN VMCM1; ACTIVATING EFFECT).
/FIId-VAR_008716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENDOTHELIAL CELLS. SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
                                                                                                          (POTENTIAL)
(POTENTIAL)
                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 2 IMMUNOSLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                         DB 1; Length 1124;
                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                   65BC05D18FA4CCEC CRC64;
             DOMAIN 2.
                                                    PROTEIN KINASE.

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

N-LINED (GLCNAC...) (
N-LINKED (GLCNAC...) (
            IG-LIKE C2-TYPE DOMAIN 2 FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2. FIBRONECTIN TYPE-III 3.
                                                                                                                                                                                            (AUTO-)
                                                                                                                                                                                               PHOSPHORYLATION
                                                                                                                                                                                                                                                                         Score 35; DB :
Pred. No. 54;
1; Mismatches
  EGF-LIKE 3.
                                                                                                                                                                                                                                                   1124 AA; 125810 MW;
                                                                                                                                                                                                                                                                                                                                                                                            TIE2_BOVIN STANDARD; 006807; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                                                                                                                                         61.4%;
60.0%;
                                                                                                                                                                                                                                                                                   Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase receptor TIE-2).
TEK OR TIE2 OR TIE-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine),
                                                                                                                                                                                                                                                                                                                                       289 CATGWKGLOC 298
                                                                                                                                                                                                                                                                                                                  1 CATDIKGAEC 10
                     NCBI_TaxID=9913;
                                                                                                                                                                                                                             897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY
                                        DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                         Query Match
                                                                                                          CARBOHYD
                                                                                                                     CARBOHYL
                                                                                                                              CARBOHYE
                                                                                                                                          CARBOHYL
                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                             VARIANT
                     DOMAIN
                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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               between the Swiss Institute of Bioinformatics and the EMBL outstation—
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-11ke domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family.

1 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 1; Length 1125;
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGF_PIG STANDARD; PRT; 229 AA.
029074.
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
NGFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POT IW; 015F1320ABB53B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
IG-LIKE C2-TYPE DOMAIN 2.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANGIOPOIETIN 1 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE
                                                                                                                                                                                                                            InterPro; 1PR000561; EGF-like.
InterPro; 1PR000719; Euk_pkinase.
InterPro; 1PR003049; Euk_pkinase.
InterPro; 1PR003049; Euk_pkinase.
InterPro; 1PR001245; Tyr_lil.
InterPro; 1PR001245; Tyr_pkinase.
Pfam; PR00049; EGF; 2.
Pfam; PR00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000001; Euk_pkinase; 1.
SMART; SM00180; EGF_like; 1.
SMART; SM00180; EGF_like; 1.
SMART; SM00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
PROSITE; PS001186; EGF_1; 3.
PROSITE; PS001186; EGF_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125927 MW;
                                                                                                                                                                 EMBL; X71424; CAA50555.1; -. PIR; S32691; S32691.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11125
746
746
1771
102
252
252
299
341
424
538
635
730
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730
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1125 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CATDIKGAEC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                Labbb-Mansais Y., Mellink C., Yerle M., Gellin J.;

"A new marker (NGFB) on pig chromosome 4, isolated by using a consensus sequence conserved among species.";

Cytogenet. Cell Genet. 67:120-125(1994).

-I- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT EMBRYONIC SENSORY NEURONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 34; DB 1; Length 229; 87.5%; Pred. No. 20; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                         -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BETA-NERVE GROWTH FACTOR.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (PC
FE8890771CBA3189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                       SEQUENCE FROM N.A.
STRAIN-Large white; TISSUE-Blood;
MEDLINE-94313891; Pubmed-8039422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 N
25275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00248; NGF_1; 1.
PROSITE; PS50270; NGF_2; 1.
Growth factor; Signal.
NON_TER 1 1
SIGNAL < 1 6
PROPEP 7 109
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L31898; AAA21301.1; -.
HSSP; P01139; 1BET.
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002072; NGF. Pfam; PF00243; NGF; 1. ProDom; PD002052; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
109
229
189
217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00140; NGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
102
154
229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

Search completed: November 9, 2002, 14:01:44 Job time: 8.69231 secs

j.

2 ATDIKGAE 9 |||||| | 137 ATDIKGKE 144

do Db

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

November 9, 2002, 13:59:34; Search time 13.8462 Seconds. (without alignments) 69.430 Million cell updates/sec Run on:

US-09-632-748-9 57 1 CATDIKGAEC 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | mom - Catotototo | Processi
Defical nro | ubjanitin thiolest | notch protein - fr | 2 | spholipase A | | phospholipase A2 | | | Tat-binding protes | hypothetical prote | | hypothetical prote | Ca2+-transporting | protein-tyrosine k | protein-tyrosine k | hypothetical prote | Id heavy chain V r | nerve growth facto | | | growth | growth | growth | Jerve or | C 3.4.25 1 protess | ve growt | |
|-----------|---------------|------------------|-------------------------|--------------------|--------------------|--------|--------------|--------|------------------|-------|--------|--------------------|--------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|----------|--------------------|----------|--------|
| SUMMARIES | ID | T42049 | T34254 | T09478 | A24420 | S20773 | PSLT3E | PSLT4E | PSLT1E | PSOXA | F95945 | A34832 | T33155 | T18974 | T22933 | T04172 | 158388 | S57846 | T15961 | S08462 | A26312 | H71811 | 146614 | S14481 | JE0097 | A26311 | 156570 | B55904 | NGHUBM | D42586 |
| | DB | 7 | 7 | 7 | _ | C) | | - | Н | - | 7 | 7 | ~ | | | | | | | | | 7 | 7 | a | ~ | 7 | 7 | 7 | _ | ~ |
| | Length | 362 | 381 | 963 | 2703 | 40 | 118 | 118 | 118 | 119 | 271 | 404 | 430 | 939 | 965 | 1048 | 1124 | 1125 | 1456 | 103 | 125 | 227 | 229 | 235 | 241 | 243 | 245 | 254 | 286 | 289 |
| dю | Query | 66.7 | 66.7 | 66.7 | • | 64.9 | 61.4 | _ | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 61.4 | 60.5 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 | 59.6 |
| | Score | 38 | 38 | 38 | 38 | 37 | 35 | 32 | 32 | 32 | 32 | 32 | 35 | 35 | 32 | 35 | 35 | m | 34.5 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 |
| | Result
No. | н | 7 | က | 4 | S | 9 | 7 | æ · | on I | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 |

| A a near + [Waccontinuin] & | dlucuronosyltransf | sidea-B roallator | nerve growth facto | Asparaciparacis | | RNA 3'-terminal ph | probable cell | ATD-CARE COLL GLOW | hypothotical pacto | | | | hursthetter proce | nypornerical prote | protein F11C7.4 [1 | estrogen receptor |
|-----------------------------|--------------------|-------------------|--------------------|-----------------|--------|--------------------|---------------|--------------------|--------------------|--------|--------|--------|-------------------|--------------------|--------------------|-------------------|
| C42586 | B42586 | F75620 | NGMSMG | S18999 | B44478 | E83072 | A44478 | JC4843 | F84615 | D89876 | T21175 | E72350 | T/7801 | T00/41 | E89753 | PW0044 |
| 2 | 7 | 7 | П | ~ | 7 | ~ | 7 | 7 | ~ | 0 | 10 | ı c | 0 | 4 | N | 0 |
| 289 | 289 | 299 | 307 | 322 | 337 | 341 | 373 | 379 | 381 | 494 | 651 | 992 | 1616 | 1 | 1722 | , 80 |
| ف | ٥ | ٥ | 9 | 9 | 9 | 9 | 9 | 9 | 9 | ع | φ | 9 | ی | , | ٩ | 6 |
| 59 | 59.6 | 59. | 59. | 59. | 59. | 59. | 59. | 59. | 59 | 59 | 20 | 59 | 0 | , | ž. | 57. |
| 34 | 34 | 34 | 34 | 34 | | | | 34 | | | | 34 | 3.4 | | 34 | |
| 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | | 44 | 45 |

ALIGNMENTS

```
RESULT 1
T42049
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Grotein - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Dec-1999 #text_change 21-Jul-2000
C.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C.Dec-1990 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C.Dec-1990 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C.Sell 90, 707-716, 1997
A.Tulcia Wht signaling and an APC related gene specify endoderm in early C. elegans e A.Reference number: 215051; MUID:97433081; PMID:9288750
A.Recession: T42049
A.Reference number: 215051; MUID:97433081; PMID:9288750
A.Recession: T42049
A.Reference number: 215051; MUID:92343266; PIDN:AAC47749.1; PID:92343267
C.Genetics:

A; Gene: mom-2

C; Superfamily: int-1 transforming protein

Gaps ö Score 38; DB 2; Length 362; Pred. No. 15; 1; Mismatches 3; Indels 66.78; Best Local Similarity 60.0 Matches 6; Conservative Query Match

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304 CAIDVKDREC 313 1 CATDIKGAEC 10 ò

g

RESULT 2 T34254

hypothetical protein F38E1.7 · Caenorhabditis elegans

C; species: Caenorhabditis elegans C; Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 21-Jan-2000 C; Accession: T34254 R; Gattung, S; Le, T. submitted to the EmBL Data Library, December 1995 A; Description: The sequence of C. elegans cosmid F38E1.

A; Accession: T34254

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-381 <GAT>
A;Cross-references: EMBL:U41996; PIDN:AAA83472.1; CESP:F38E1.7

C;Genetics:

A; Gene: CESP:F38E1.7 A; Introns: 26/2; 69/3; 105/1; 131/3; 288/3; 346/3 C; Superfamily: int-1 transforming protein

Length 381; 3; Indels Query Match 66.7%; Score 38; DB 2; Best Local Similarity 60.0%; Pred. No. 16; Matches 6; Conservative 1; Mismatches 5

ö

Gaps

; 0

엄 δ

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A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A; Note: the reaction is strongly enhanced when the phospholipid is condensed into a m C; Superfamily: phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Accession: A00753
C. Accession: A00753
R. Nishida, S.; Kim, H.S.; Tamiya, N.
Biochem. J. 207, 589-584, 1982
A. Title: Amino acid sequences of three phospholipases A I, III and IV from the venom A; Reference number: A90316; MUD:83153048; PMID:7165712
A. Recession: A00753
A. Molecule type: protein
A. Residues: 1-118 CNIS>
C. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Corporate: 20-7073
R.Mortari, F.; Wang, J.; Schroeder, H.W.
Submitted to the RMEL Data Library, April 1992
A.Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A.Recession: S20764
A.Recession: S20773
A.Molecule type: DNA
A.Residues: 1-40 < MOR>
A.Residues: 1-40 < MOR>
A.Cross-references: EMBL: Z11944; NID:g33878; PIDN:CAA78001.1; PID:g33879
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin immunoglobulin
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N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Laticauda semifasciata (broad-banded blue sea krait, erabu sea snake)
C;Date: 02-Apr-1982 #sequence_revision 13-Jun-1983 #text_change 28-Feb-1997
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2436/3; 2588/3
C;Superfamily: notch protein; ankyrin repeat; transmembrane protein
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: EGF homology CEGX1>
F;297-328/Domain: EGF homology CEGX1>
F;530-561/Domain: EGF homology CEGX1>
F;580-594/Domain: EGF homology CEGY2>
F;1064-1095/Domain: EGF homology CEGY3>
F;108-1218/Domain: EGF homology CEGY3>
F;108-1218/Domain: EGF homology CEGY3>
F;108-1218/Domain: EGF homology CEGY3>
F;108-1218/Domain: ankyrin repeat homology CANI>
F;108-2015/Domain: ankyrin repeat homology CANI>
F;2017-2049/Domain: ankyrin repeat homology CANI>
F;208-2165/Domain: ankyrin repeat homology CANI>
F;208-2168/Region: glutamine-rich
F;2538-2568/Region: glutamine-rich
F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted COPA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 38; DB 1; Length 2703; 60.0%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.9%; Score 37; DB 2; Length 40; 60.0%; Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (VH3, IN48P1) - human (fragment)
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Best Local Similarity 60.00
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Best Local Similarity
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8 CTTDLGGAYC 17
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A; Reference number: S09358; MUID:89385974; PMID:2780284
A; Accession: S09358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-2703 (KLD>
A; Residues: 1-2703 (KLD>
A; Residues: 1-2703 (KLD>
A; Cross-references: (B: KO3508; NID:g157991; PIDN:AAA28725.1; PID:g157993
B; Whatton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A; Reference number: A24768; MUID:86079539; PMID:3935325
A; Accession: A24768
A; Molecule type: mRNA
A; Residues: 1-48, I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, A; Mole: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
B; Tautz, D.
Nucleic Acids Res, 17, 6463-6471, 1989
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A; Readduces: 2505-2551, 00000, 2552-2576, 'E', 2578-2604 <TAU>
A; Readduces: 2505-2551, 00000, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A; Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
A; Reference number: A05267; MUID: 85099329; PMID: 2981631
A; Accession: A05267
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C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24420; A24768; S09358; A05267
R;Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A;Reference number: A24420; MUID:87064624; PMID:3097517
                                                                                                                                                                                                                                                   ubiquitin thiolesterase (EC 3.1.2.15) - human N;Alternate names: ubiquitin carboxy-terminal esterase (Species: Homo sapiens (man) c.Species: Homo sapiens (man) c.pate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A) Residues: 1-963 <GRA>
A)Cross-references: EMBL:U20657; NID:g2459396; PID:g2459395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: Z16684
A;Accession: T09478
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notch protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 3
C,Keywords: proto-oncogene; thiolester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                  R,Gray, D.A.
submitted to the EMBL Data Library, October 1997
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A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.7%;
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568 CSTSVDGSEC 577
                                                                                     304 CAIDVKDREC 313
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                     1 CATDIKGAEC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A24420
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                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T09478
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predicted

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Gaps

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2; Indels

3; Mismatches Score 35; Pred. No.

1 CATDIKGAEC 10

õ qq

89 CACDLEAAKC

RESULT 9

61.4%; 50.0%;

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F;4,67/Binding site: micellar substrate (Gln, Tyr) #status predicted F;11-71,27-117,29-45,44-98,51-91,60-84,78-89/Disulfide bonds: #status predi F;28,30,32,49/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted F;48,92/Active site: His, Asp #status predicted
                                                                                                                                                                                  Ouery Match
Best Local Similarity 50.07
الموافقة 5, Conservative
C.Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pred
                                                                                                   predicted
                                  F;4,67/Binding site: micellar substrate (Gln, Tyr) #status predicted F;11-71,27-117,29-45,44-98,51-91,60-84,78-89/Disulfide bonds: #status pred F;28,30,32,49/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted F;48,92/Active site: His, Asp #status predicted
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ö ö Score 35; DB 1; Length 118; Pred. No. 21; 2; Indels 3; Mismatches Pred. No. 61.4%; 50.0%; 5; Conservative Local Similarity Query Match Matches

1 CATDIKGAEC 10 δ

89 CACDLEAAKC 98

RESULT 7

phospholipase A2 (EC 3.1.1.4) IV - broad-banded blue sea krait

N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Specias: Laticauda semifasciata (broad-banded blue sea krait, erabu sea snake)
C;Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Feb-1997
C;Accession: A90316; A00753
B;Nishida, S; Kin, H.S; Tamiya, N.
Biochem. J. 207, 589-594, 1982
A;Title: Amino acid sequences of three phospholipases A I, III and IV from the venom of A;Reference number: A90316; MUID:83153048; PMID:7165712

phospholipase A2 (EC 3.1.1.4) taipoxin alpha chain - Australian taipan
N.Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-Feb-1997
C;Accession: A00754
R/Lind, P.; Earker, D.
Eur. J. Biochem. 124, 441-447, 1982
A;Title: Amino-acid sequence of the alpha-subunit of taipoxin, an extremely potent pr

A posseription: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a m C;Superfamily: phospholipase A2
C;Superfamily: phospholipase A2
C;Superfamily: acrosylic ester hydrolase; lipid degradation; metalloprotein; p F;4,68/Binding site: micellar substrate (Gln, Tyr) #status predicted
F;1-72,27-118,29-45,44-99,151-92,61-85,79-90/Disulfide bonds: #status predicted
F;28,30,32,49/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F;48,93/Active site: His, Asp #status predicted

A; Molecule type: protein A; Residues: 1-119 <LIN>

C; Function:

A; Accession: A00754

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Gaps

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4; Indels

DB 1; Length 119;

Score 35; DB Pred. No. 21; 0; Mismatches

61.4%; 60.0%;

6; Conservative

1 CATDIKGAEC 10

δλ qq

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Gaps

90 CRCDAKAAEC

Best Local Similarity

Matches

Query Match

A; Accession: A90316 A; Molecule type: protein A; Residues: 1-118 <NIS>

A pescription: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-shoser the reaction is strongly enhanced when the phospholipid is condensed into a mice (Signamily: phospholipase A2. (Signamily: phospholipase A2. (Signamily: phospholipase A2. (Signamily: phospholipase A3. (Signamily: Signamily: Signamily:

DB 1; Length 118; 2; Indels 3; Mismatches Pred. No. 21; Score 35; 61.4%; 50.0%; Conservative Best Local Similarity Query Match Matches

1 CATDIKGAEC 10 ò

89 CACDLEAAKC 98 g

phospholipase A2 (EC 3.1.1.4) I - broad-banded blue sea krait
N;Alternate names: phosphatidylcholine 2-acylhydrolase
C;Species: Laticauda semifascilata (broad-banded blue sea krait, erabu sea snake)
C;Date: 02-Apr-1882 #sequence_revision 31-Dec-1989 #text_change 28-Feb-1997
C;Accession: A94325; A00752; A30821
Toxicon 26, 747-749, 1988
A;Title: Correction of amino acid sequence of phospholipase A-2 I from the venom of Lati

A; Accession: A94325

A; Molecule type: protein A; Residues: 1-118 <TAK>

Rinishida, S.; Kim, H.S.; Tamiya, N. Blochem. J. 207, 589-594, 1982
Blochem. J. 207, 589-594, 1982
A:Title: Amino acid sequences of three phospholipases A I, III and IV from the venom of A:Reference number: A90316; MUID:8153048; PMID:7165712
A;Contents: annotation; specific activity
A;Note: Trp-64 is important to enzyme activity
C;Function:

A)Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

probable formimidoylglutamase (EC 3.5.3.8) [imported] - Sinorhizobium meliloti (strai C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 03-Jun-2002 C;Accession: F95945

Rifinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Titler The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e A;Reference number: A95842; MUID:21396508; PMID:11481431

A; Status: preliminary

A Molecule type: DNA A; Residues: 1-271 <KUR> A; Cross-references: GB:AL591985; PIDN:CAC49230_1; PID:915140716; GSPDB:GN00167

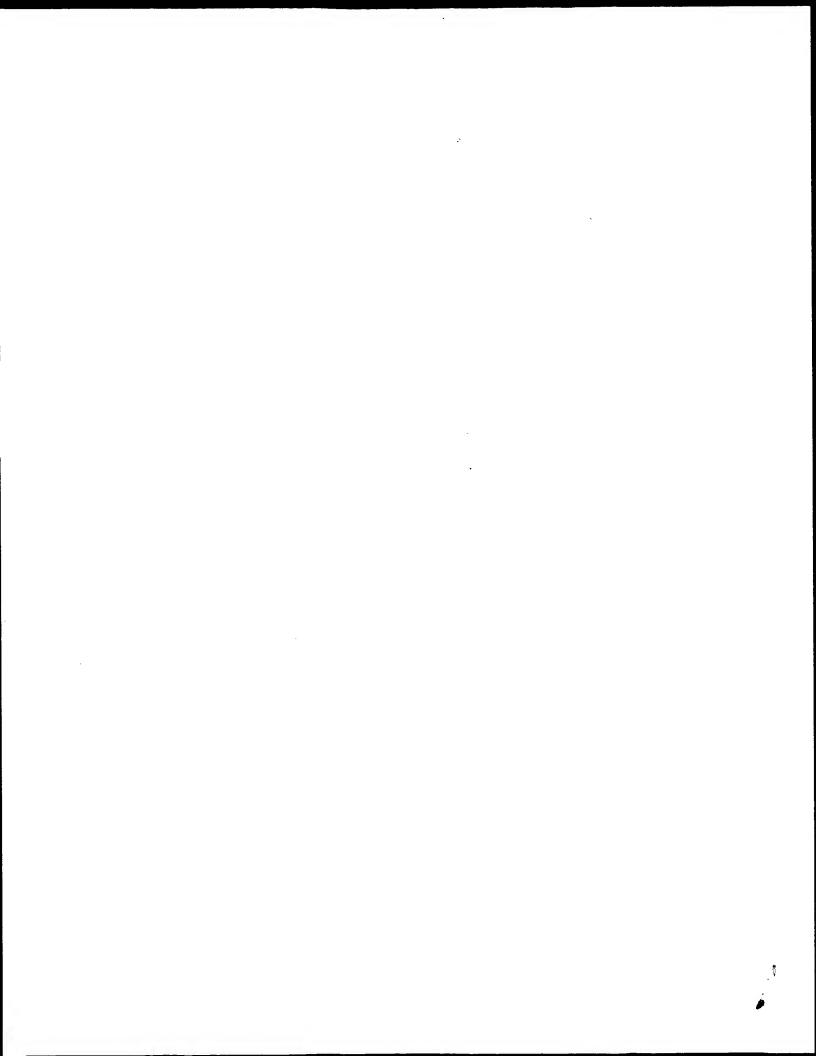
A; Experimental source: strain 1021, megaplasmid psymB R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A.Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizoblum meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics:

```
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-Apr-2002
R;Chen, X: Chang, M.; Wang, B.; Wu, B.
R;Chen, X: Chang, M.; Wang, B.; Wu, B.
A;Title: Cloning of a Ca(2+)-ATPase gene and the role of cytosolic Ca2+ in the gibber A;Title: Cloning of a Ca(2+)-ATPase gene and the role of cytosolic Ca2+ in the gibber A;Accession: 10412
A;Accession: 10412
A;Accession: 10412
A;Accession: Total are a Ca2+ in the gibber A;Accession: Total are a Ca2+ in the gib
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A;Introns: 52/3; 116/2; 172/3; 308/1; 550/2; 609/1; 665/2; 723/3; 805/3; 927/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 52/3; 116/2; 146/3; 282/1; 524/2; 583/1; 639/2; 697/3; 779/3; 901/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: 219639
A;Accession: T22933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-965 - WAIL>
A;Experimental source: clone F58G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;cross-references: EMBL:Z49886; PIDN:CAA90054.1; GSPDB:GN00020; CESP:C06A1.4
A;Experimental source: clone C06A1
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22933
R;Smye, R.
submitted to the EMBL Data Library, November 1996
                                                                                        hypothetical protein C06Al.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18974
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60.0%; Pred. No. 1.3e+02;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1995
A;Reference number: 219054
A;Accession: T18974
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-939 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ca2+-transporting ATPase (EC 3.6.3.8) - rice
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Best Local Similarity 60.vv
....a 6; Conservative
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343 CAAVIKGLDC 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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A; Residues: 1-404 <NEL>
A; Cross-references: GB:M34079; NID:g338699; PIDN:AAA36666.1; PID:g338700
A; Cross-references: GB:M34079; NID:g338699; PIDN:AAA36666.1; PID:g338700
C; Superfamily: ATP-dependent 26S proteinase; FtsH/SEC18/CDC48-type ATP-binding domain hc
C; Keywords: ATP; nucleotide binding; P-loop
F;165-375/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>
F;192-199/Region: nucleotide-binding motif A (P-loop)
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A;Introns: 221/1; 318/3; 367/2
C;Superfamily: ATP-dependent 265 proteinase; FtsH/SEC18/CDC48-type ATP-binding domain hd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A34832
R; Nelbock, P.; Dillon, P.J.; Perkins, A.; Rosen, C.A.
Science 248, 1650-1653, 1990
A; Title: A cDNA for a protein that interacts with the human immunodeficiency virus tat
A; Reference number: A34832; MUID:90302011; PMID:2194290
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A; Cross-references: EMBL:AF067618; PIDN:AAC19196.1; GSPDB:GN00019; CESP:F56H1.4
A; Experimental source: strain Bristol N2; clone F56H1
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C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
C.Accession: T33155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.bate: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 19-Jan-2001
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                                                                                                                                                                                            Length 271;
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                                                                            C;Superfamily: Yersinia pestis hypothetical protein hutG
C;Keywords: hydrolase
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A;Description: The sequence of C. elegans cosmid F56Hl.
A;Reference number: 221293
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Best Local Similarity 50.vv
Thes 5; Conservative
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A; Residues: 1-404 <NEL>
A;Gene: hutG; SMb21164
A;Genome: plasmid
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A; Status: preliminary
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A;Cross-references: EMBL:U82966; NID:g2160711; PIDN:AAB58910.1; PID:g2160712
A;Experimental source: cv.IR36
C;Genetics:
A:Introns: 444/3; 521/3; 615/3; 729/3; 779/3; 854/3
C;Genetics:
A:Introns: 444/3; 521/3; 615/3; 729/3; 779/3; 854/3
C;Superfamily: Na+/K+transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: Na+/K+transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: Na+/K+transporting are redicted <CA>
C;Keywords: hydrolase; phosphoprotein
C;Keywords: hydrolase; phosphoprotein
F;39-56/Domain: calcium binding #status predicted <CA>
F;36-256/Domain: calcium binding #status predicted <CA4>
F;317-386/Domain: calcium binding #status predicted <CA4>
F;513-696/Domain: ATP binding #status predicted <ATP>
F;610-784/Domain: ATP binding #status predicted <CA5>
F;610-784/Domain: calcium binding #status predicted <CA5>
F;358-ACTic/Domain: Calcium binding #status predicted <CA5>
F;358-ACTic/Bomain: calcium binding #status predicted <CA5>
F;358-ACTic/Bomain: ASP (aspartylphosphate intermediate) #status predicted
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Search completed: November 9, 2002, 14:03:43 Job time: 14.8462 secs



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9, 2002, 14:03:09; Search time 6.15385 Seconds (without alignments) 23.430 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Total number of hits satisfying chosen parameters: 92612 seqs, 14418503 residues Gapop 10.0 , Gapext 0.5 US-09-632-748-9 57 1 CATDIKGAEC 10 **BLOSUM62** Perfect score: Scoring table: Searched: Sednence:

Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 1, Appli Sequence 4, Appli Sequence 6, Appli Sequence 8, Appli Sequence 53, Appli Sequence 11521, A Sequence 11521, A Sequence 13, Appli Sequence 1821, A Sequence 21, Appli Sequence 3, Appli Sequence 3, Appli Sequence 52, Appli Sequence 4, Appli Sequence 6, Appli Sequence 8, Appli Sequence 5, Appli Sequence 16, Appli 6, Appl Appli Appli Appli Description US-09-822-263-16
US-10-072-681-1
US-09-305-856B-4
US-09-305-856B-6
US-09-305-856B-6
US-09-919-497-53
US-09-808-4-10315
US-09-808-602-13
US-09-808-602-13 0.05-09-848-664-21 2.05-10-072-681-3 2.05-10-072-681-3 0.05-09-72-681-3 0.05-09-798-338-4 0.05-09-798-338-4 0.05-09-798-338-6 0.05-09-798-338-8 0.05-09-798-338-8 Query Match Length DB Score Result

| Sequence 80, Appl
Sequence 84, Appl
Sequence 149, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 2, Appl 1
Sequence 2, Appl 1
Sequence 28, Appl 1
Sequence 28, Appl 1
Sequence 27, Appl 1 | Sequence 11137, A |
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| US-09-808-602-80
US-09-808-602-84
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US-10-001-843-149
US-09-864-761-46197
US-10-036-342-61
US-10-036-342-61
US-10-036-342-61
US-09-915-593-2
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US-09-915-593-2
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ALIGNMENTS

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APPLICANT: SALIYAMA Elbert, Shelly E. APPLICANT: SALIYAMA Elbert, Shelly E. APPLICANT: Hubbell, Jeffrey A. TITLE OF INVENTION: Controlled Release of No. US20020146414Al-Heparin Binding Grow TITLE OF INVENTION: Factors from Heparin Containing Matrices FTH 108 CURRENT APPLICATION NUMBER: US/09/848,664 CURRENT APPLICATION NUMBER: US/09/848,664 PRIOR APPLICATION NUMBER: 09/298,084 PRIOR FILING DATE: 1999-04-22 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.1
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                ; Sequence 21, Application US/09848664; Patent No. US20020146414A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-848-664-21
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LENGTH: 72
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Sequence 2, Application US/10072681
Patent No. US20020137893A1
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Brek, Joanne T.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REPERENCE: GENENT.037C3
CURRENT APPLICATION NUMBER: US/10/072,681 RESULT 2 US-10-072-681-2

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APPLICANT: ROSENTHAL, ARNON
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APPLICANT: Schwelzer, Charles H.
APPLICANY: Burton, Louis E.
APPLICANY: Beck, Joanne T.
APPLICANY: Beck, Joanne T.
TITLE OF INVERTION: PURIFICATION OF NGF
FILE REFERENCE: GENENT.037C3
CURRENT APPLICATION NUMBER: 08/10/072,681
CURRENT APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR FILING DATE: 1997-05-29
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASLSEQ FOR WINDGWS Version 4.0
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1966-11-15
PRIOR PELICATION NUMBER: 60/047855
PRIOR APPLICATION NUMBER: 60/047855
PRIOR APPLICATION NUMBER: 08/970865
PRIOR APPLICATION NUMBER: 09/363573
PRIOR APPLICATION NUMBER: 09/363573
PRIOR APPLICATION NUMBER: 09/675,503
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 6
SOFTHARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10072681 Patent No. US20020137893A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapien
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ORGANISM: mouse
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US-08-450-842-52
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LENGTH: 121
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APPLICANT: Satiyama, Shelly E.
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF PROTEINS
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/141,153
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATCHIN VET. 2.00
SEQ ID NO 2
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TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,842
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                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/426419
FILING DAME: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DAME: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/68482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY AGENT INFORMATION:
NAME: TOTCCHIA, TIMOCRAMATION:
NAME: TOTCCHIA, TIMOCRAMION:
TELEDHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09798338 ; Patent No. US20010020086A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 52:
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TOPOLOGY: 11-1
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; APPLICANT: Hubbell, Jeffrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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US-09-798-338-2
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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LENGTH: 167
TYPE: PRT
ORGANISM: Artificial Sequence
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72 ATDIKGKE 79
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76 ATDIKGKE 83
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US-09-798-338-8
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US-08-450-842-5
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Patent No. US20010020086A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: SALYARA, SALIY E.
TITLE OF INVENTION: ENGINEERING: INCORPORATION OF FIBRIN FOR TISSUE;
TITLE OF INVENTION: ENGINEERING: NOOPPORTION OF PROTEINS
FILE REFERENCE: 87662-68879
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VOICE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hubbell, Jeffrey A.
APPLICANT: Schense, Jason C.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENGINEERING: INCORPORATION OF FIBRIN FOR TISSUE
TITLE OF INVENTION: ENGINEERING: INCORPORATION OF PROTEINS
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 09/141,153
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 163
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                                                                         OTHER INFORMATION: Description of Artificial Sequence:Artificial OTHER INFORMATION: Protein Sequence
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                                                                                                                                                          59.6%; Score 34; DB 10; Length 153; 87.5%; Pred. No. 14; vative 0; Mismatches 1; Indels
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Pred. No. 14;
0; Mismatches 1; Indels
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                                     ORGANISM: Artificial Sequence
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Best Local Similarity 87.53
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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LENGTH: 153
                                                                                                                    US-09-798-338-2
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Gaps
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APPLICANT: Schense, Jason C.
APPLICANT: Schense, Jason C.
APPLICANT: Schense, Jason C.
APPLICANT: Sakiyama, Shelly E.
TITLE OF INVENTION: ENGINEERING: INCORPORATION OF FIBRIN FOR TISSUE
TITLE OF INVENTION: ENGINEERING: INCORPORATION OF PROTEINS
TITLE OF INVENTION: ENGINEERING: INCORPORATION OF PROTEINS
FILE REFERENCE: 87662-68879
CURRENT APPLICATION NUMBER: US/09/798,338
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
; OTHER INFORMATION: Description of Artificial Sequence:Artificial is OTHER INFORMATION: Protein Sequence US-09-798-338-6
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                                                                                                                                           Query Match 59.6%; Score 34; DB 10; Length 163; Best Local Similarity 87.5%; Pred. No. 15; Matches 7; Conservative 0; Mismatches 1; Indels
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Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: RESENTHAL, ARNON
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.25 inch, 360 Kb floppy disk
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,842

FILING DATE:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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; Patent No. US20010020086A1
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Gaps
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                       Gaps
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Patent No. US20020061518A1

GENERAL INFORMATION:
APPLICANT: Penny, Laura
APPLICANT: Penny, Laura
TITLE OF INVENTION: Genctyping the Human
TITLE OF INVENTION: UDP-Glucuronosyltransferase 1 (UGT1) Gene
TITLE OF INVENTION: UDP-Glucuronosyltransferase
CURRENT APPLICATION NUMBER: US/09/305,856B
CURRENT FILING DATE: 1999-05-05
PRIOR PILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 289
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                                                                                                                                                                                                       Sequence 1, Application US/10072681
Sequence 1, Application US/10072681
FREATH NO. US20020137893A1
GENERAL INFORMATION:
APPLICANT: BUTTON, LOUIS E.
APPLICANT: BECK, JOANNE T.
TITLE OF INVENTION: PURIFICATION OF NGF
FILE REFERENCE: GENERY.037C3
CURRENT APPLICATION NUMBER: US/10/072,681
CURRENT APPLICATION NUMBER: 05.008
FRIOR FILING DATE: 1996-11-15
FRIOR FILING DATE: 1997-05-29
FRIOR FILING DATE: 1997-11-14
FRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 6
SOFWMARE: FEALESED for Windows Version 4.0
Pred. No. 21;
0; Mismatches
Best Local Similarity 87.5%;
Matches 7; Conservative
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Matches 7; Conservative
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ORGANISM: Homo sapiens
US-09-305-856B-4
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US-10-072-681-1
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Matches 5; Conserva
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149 ATDIKGKE 156
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US-09-305-856B-4
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US-10-072-681-1
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APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Spidek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Treperney, Veliar T
TITLE OF INVENTION: No. US20020036598alel Polynucleotides and Polypeptides Encoded TH
FILE REFERENCE: 15966-572 CIP1
CURRENT APPLICATION NUMBER: 09/672,665
PRIOR APPLICATION NUMBER: 09/672,665
PRIOR PAPLICATION NUMBER: 60/156,745
PRIOR PAPLICATION NUMBER: 60/156,745
PRIOR APPLICATION NUMBER: 60/159,248
PRIOR APPLICATION NUMBER: 60/159,248
PRIOR APPLICATION NUMBER: 60/159,344
PRIOR APPLICATION NUMBER: 60/159,344
PRIOR PILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 60/215,048
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 36
SSOFTWARE: PALENTIN Ver: 2.1
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Pred. No. 21;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                 666P2C1D3
                                            PROFICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-822-263-16
Sequence 16, Application US/09822263
Patent No. US20020036598A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Vernet, Corine
                                                                                                                                                                                                                                                                                                                NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2
TELECOMMUNICATION INFORMATION:
TELEPAX: 415,725-8674
TELEX: 910,731-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.68;
87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 241 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                            This invention describes novel agonists (competitive inhibitor) and/or inhibitors of amyloid formation peptides which are 3-15 amino acids in length and contain at least the active sequence GA. The new peptides are useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of type II diabetes mellitus, Alzheimer's disease and spongiform encephalopathies (e.g. CJD, scrapie and BSE).
                                                                                                                                                                                           Gaps
                   Peptides containing amino acid sequence GA - useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of type II diabetes mellitus
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                                                                                                                                                                    100.0%; Score 15; DB 20; Length 8; 100.0%; Pred. No. 7.8e+05; Ive 0; Mismatches 0; Indels
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                                                          Claim 5; Column 5; 8pp; German.
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                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                           DE19725619 peptide #13.
WPI; 1999-121938/11.
                                                                                                                                                  8 AA;
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Best Local S
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                                                                                                                                                                                                                                                             RESULT 45
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BSE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agonist; cytotoxic; competitive inhibitor; amyloid formation; type II diabetes mellitus; Alzheimer's disease; CJD; scrapie; spongiform encephalopathy.
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Length 8;

Score 15; DB 20; Pred. No. 7.8e+05;

100.0%; 100.0%;

Query Match 'Best Local Similarity

8 AA;

Sequence

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Gaps
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Indels
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Mismatches
                                                               9, 2002, 14:12:36
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Conservative
                                                               Search completed: November
                                                                        Job time : 36 secs
3;
                1 KGA 3
                                   2 KGA 4
Matches
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DE19725619-A1
              03-FEB-1999;
                                         04-FEB-1998;
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                                                                                                Eller M,
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                                                                                                                                                                                                                                                                         This sequence represents a molecular mimetic of a unique epitope of Neissria meningitidis serotype B (MenB). This sequence was isolated using the antibodies (Ab) of the invention. The Ab are directed against a MenB capsular polysaccharide (PS) derivative, and are not autoreactive. The Ab either do not cross-react or they are minimally cross-reactive. The Ab either do not cross-react or they are minimally cross-reactive. The Ab either do not cross-react or they are minimally cross-reactive. The non-autoreactive Ab are particularly useful for identifying molecular mimetics of unique MenB PS epitopes that can be used in vaccine compositions. Furthermore, the Ab, humanised on the Ab, crompositions. Furthermore, the Ab, humanised on the Ab, fragments and functional equivalents, will also find use in passive immunisation against, and/or as an adjunct to therapy for, MenB and Escherichia coli Kil disease. Such disease includes bacterial meningitis and sepsis in infants, children and adults. The anti-MenB Ab can also be used to investigate the bactericial and/or opsonic function of Ab of different specificities, as well as to identify the molecular nature of the unique epitopes on the MenB bacterial surface that are not cross-reactive with host PS. The anti-MenB Ab can be used to isolated fractions of MenB bacterial or MenB PS derivatives. Once isolated fractions of MenB bacteria or MenB PS derivatives. Once isolated employed directly in oligosaccharide protein conjugate vaccines or to model synthetic saccharides or mimetics for use in vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p75NTR; p75 neurotrophin receptor; nerve growth factor; NGF; melanocyte; keratinocyte; apoptosis; Bc1-2; beta-amyloid fragment; Alzheimer's disease; pseudo-ligand; hair growth; hair colour; skin colour; alopecia areata; male pattern baldness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-amyloid fragment for generation of p75NTR inhibiting peptides
                                                                                                                                                                                            Antibodies to Neisseria meningitidis serotype B - prepared using capsular polysaccharide derivatives, used to develop products for treating or preventing infections, e.g. meningitis and sepsis
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                  Claim 17; Fig 7A; 109pp; English.
                                                     97WO-US15167.
                                                                                 96US-0025799
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Best Local Similarity 100.

Matches 3; Conservative
                                                                                                             (CHIR ) CHIRON CORP.
                                                                                                                                                                   WPI; 1998-216938/19
                                                                                                                                        Granoff D, Moe GR;
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WO9808874-A1
                                                      27-AUG-1997;
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                            05-MAR-1998.
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This sequence is amino acids 24-31 of beta-amyloid. This sequence can be used to generate cyclic peptide AAY39233. The cyclic peptide competes with and competitively inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR). P75NTR is a low affinity nerve growth factor (NGF) receptor which is expressed by melanocytes and keratinocytes of the basal epidermis. Apoptosis can be inhibited by p75NTR via the upregulation of the Bal-2 protein. If the receptor is occupied by examples of appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other examples of appropriate ligands include this cyclic peptide. This peptide is based on the sequence of the binding fragment of beta-amyloid, which in methods to control or manipulate keratinocyte or melanocyte cell death. The methods involve using this peptide or peptides AAY39234-Y39235 to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting apoptosis. The new method can induce or maintain hair growth, hair colour or skin colour. Inducing or maintaining hair growth is useful for treating alopecia areata or male pattern baldness in vertebrates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 67pp; English.
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99WO-US02362.
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Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                    Gilchrest BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the isolation of a novel subgroup of the human themunodeficiency virus (HIV) type 1, designated group O. In particular, the inventors have isolated 2 new strains of the group O virus: strains VAU and DUR. Strain VAU was isolated from a French ALDS patient and has homology to the recently characterised Cameronian HIV strains ANT70 and WPS180. The DUR strain was isolated from a scropositive patient from the Camerons who showed atypical seroreactivity. The peptides AAW07225-30 represent peptides derived from the strain DUR gpl20 protein V3 loop. The DNA and protein sequences are used to generate peptides for detection of antibodies from patients infected with the new group O strains, as well as primers and probes to detect the viral nucleic acid sequences derived from these strains are able to distinguish between the group O and group M viral strains.
                                                                                                                    Human immunodeficiency virus; subgroup; strain; AIDS; homology; envelop; gpl20; gp41; seropositive; antibody; primer; probe; group 0; group M.
                                                                                                                                                                                                                                                                                                                                                                      New antigenic HIV-1 group O strain proteins and related nucleic acids - useful in diagnosis, vaccines, therapy etc., of infection by HIV-1 group O strains VAU or DUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;
                                                                                             HIV-1 group O strain DUR peptide (13) derived from gp120 V3 loop.
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Donjon de Saint-Martin J, Montagnier L, Quillent C;
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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                                                                                                                                                      Human immunodeficiency virus type 1.
                     AAW07226 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 58; 108pp; French
                                                                                                                                                                                                                             95WO-FR01391,
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                                                                                                                                                                                                                                                               94FR-0012554.
                                                                      (first entry)
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                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                WPI; 1996-230610/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA;
                                                                                                                                                                              WO9612809-A2
                                                                                                                                                                                                                           20-0CT-1995;
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                                                                      09-APR-1997
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5 KGA 7
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                                              AAW07226;
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RESULT 40
            AAW07226
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Degining and the end of the fragment. The invention relates to the beginning and the end of the fragment. The invention relates to a new method for evaluating the risk of an individual to develop Alzheimer's disease using cultured neural creat-derived melanocytes. Also disease using cultured neural creat-derived melanocytes. Also described are methods of therapy for Alzheimer's disease using peptides (AM45543-6) that bind to the neurotrophin receptor p75 nerve growth factor receptor (MGFR) and competitively inhibit the binding of a beta-amyloid to the p75 NGFR. The methods can be used for disgnosing and rediating Alzheimer's disease and other neurodegeneration of the low affinity NGFR localised on neural cell surfaces, such as autoimmune enclated by beta-amyloid protein, or by aberrant activation of the low affinity NGFR localised on neural cell surfaces, such as autoimmune concephicompetitis, Huntington's disease, cortico-basal degeneration, progressive supra-nuclear palsy, Gerotman-Shaussless Scheinker syndrome, Neimann-Pick disease, and progressive supranuclear palsy. In the firm skin biopsies, are good model cells for the study and diagnosis of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular mimetic; epitope; serotype B; MenB; capsular polysaccharide; immune disease; non-autoreactive antibody; vaccine; passive immunisation; Escherichia coli KI disease; bacterial meningitis; sepsis; oligosaccharide protein conjugate vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents residues 24 to 31 of beta-amyloid. A cyclic peptide was synthesised by attaching two cysteine residues to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evaluating risk of individual to develop Alzheimer's - uses cultured epidermal melanocyte(s), also useful for developing therapies for neuro-degenerative diseases
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neurotrophin receptor p75; p75NTR; cyclic.
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Best Local Similarity 100.00
'-hos 3; Conservative
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Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilchrest BA,
                                                                                                     Homo sapiens.
                                                                                                                                                                          WO9737228-A1.
                                                                                                                                                                                                                                                                                                                28-MAR-1997;
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                                                                    Synthetic.
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8 AA;
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                                                               8 AA;
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2 KGA 4
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                                                                                                                                                    similarity with bovine serum albumin (BSA). These regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated
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                                                                                                                                           Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuro-endocrine protein antigen PM-1 - useful for treating
                                                                                      Neuro-endocrine protein antigen PM-1 - useful for treating
                                                                                                                                                                                                                                                                             Length 8;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 14;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                 auto:immune diseases e.g. type I diabetes
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                                                                                                                     Claim 20; Page 38; 56pp; English.
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                                           Pietropaolo M;
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                      (JOSL-) JOSLIN DIABETES CENT.
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92US-0901523.
92US-0901523.
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                                                                                                                                                                                                                                                                                                   3; Conservative
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                                                               WPI; 1993-167624/20
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                       8 AA;
                                           Eisenbarth GS,
19-JUN-1992;
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levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PW-I protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
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PM-1; bovine serum albumin; BSA; epitope.
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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92US-0901523.
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Matches 3; Conserv
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Best Local Similarity
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29-OCT-1992;
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2 KGA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or exthremoyerins, but may also be modular receptors. The present sequence is a fragment of protein encoded by a Streptomyces chrysomallus actinomycin blosynthesis gene which was used in a plasmid in the exemplification of
                                                                                                                                                                                                                                                                                                                                 Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector
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                                                                                                                                                                                                                                                                                             S chrysomallus actinomycin biosynthase protein acmA fragment #6.
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                                                                                                                                                              AAM47142 standard; Peptide; 7 AA
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                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces chrysomallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-049276/06.
N-PSDB; ABA03322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200181564-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schauwecker F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention.
                                                                                                                                                                                                                                                     12-FEB-2002
             1 KGA 3
||||
3 KGA 5
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||||
3 KGA 5
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                                                                                                                                                                                                           AAM47142;
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                                                                                                                      RESULT 35
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Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
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                                                                                                                                                  Neuroendocrine; antigen; diabetes mellitis; pancrease; insulinoma; PM-1; bovine serum albumin; BSA; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuroendocrine; antigen; diabetes mellitis; pancrease; insulinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 15; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuro-endocrine protein antigen \mathsf{PM}\text{-}1 - useful for treating auto:immune diseases e.g. type I diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PM-1; bovine serum albumin; BSA; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR37285 standard; Protein; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JOSL-) JOSLIN DIABETES CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0788118.
92US-0901523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92WO-US09428
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06-SEP-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-167624/20.
                                                                              PM-1/BSA peptide.
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Gaps

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vector, that encodes one or more segments of a modular polypeptide. DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of protein encoded by a Streptomyces chrysomallus actinomycin biosynthesis gene which was used in a plasmid in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modular enzyme system, cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS;
inhibitors of amyloid formation peptides which are 3-15 amino acids in length and contain at least the active sequence GA. The new peptides are useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of type II diabetes mellitus, Alzheimer's disease and spongiform encephalopathies (e.g. CJD, scrapie and BSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to the preparation of DNA, in a circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chrysomallus actinomycin biosynthase protein acmA fragment #4.
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                                                                                                                                                                                                  Length
                                                                                                                                                                                               Score 15; DB 20;
Pred. No. 7.8e+05;
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100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic, non-ribosomal peptide synthetase; polyketide synthase; actinomycin biosynthase.
                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM47140 standard; Peptide; 7 AA.
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                                                                                                                                                                                               100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                               3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-049276/06.
                                                                                                                                                                                                  Query Match
Best Local Similarity
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nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABA03318
                                                                                                                                                7 AA;
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3 KGA 5
                                                                                                                                                                                                                                                                                            KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM47140;
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                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 34
AAM47140
ID AAM47
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Matches
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    88888888
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BSE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  This is an example of a lysine donor peptide that can be utilised in novel recombinant protein polymers of the invention. Such polymers (see AAM49710-28) typically comprise a repetitive amino acid backbone of repetitive units having a collagen, fibroin, elastin or keratin motif and at least 2 enzyme recognition sequences comprising a glutamine and/or lysine capable of enzyme catalysed isopeptide formation. The polymers are capable of covalant crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. They can be used as medical adhesives and sealants, in the closure of wounds and repair of damaged tissues, prosthesis coatings, drug depots, and matrices for the transplantation of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides containing amino acid sequence GA - useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of type II diabetes mellitus
                                                                                                                                                  naturally occurring useful as medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agonist; cytotoxic; competitive inhibitor; amyloid formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes mellitus; Alzheimer's disease; CJD; scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 15; DB 19;
100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                New recombinant protein polymers - containing
                                                                                                                                                                      repetitive units for crosslinking by enzymes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDIEN.
                                                                                                                                                                                             adhesives and sealants, depots and matrices
  (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kapurniotu A;
                                                                                                                                                                                                                                            Example 9; Column 49; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bernhagen J, Brunner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE19725619 peptide #11.
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                                                                                              WPI; 1998-387091/33
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nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA;
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5 KGA 7
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                                                    Cappello J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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7 AA;
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03-JUL-1996;
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03-MAR-1994;
                                                                                                                                                                  01-NOV-1996;
                               US5824645-A.
                                                                                                                       15-APR-1993;
                                                             20-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus genus; marine snail; cone snail; omega-conopeptide; analgesia; nocloeptivo pain; neuropathic pain; neuronal tissue; conotoxin; inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction; rheumatoid arthritis; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptides AAR80371-7 are examples of lysine donor peptides which can be used to generate protein polymeric adhesion substrate (PPAS) contg. repeats of non-fibrin cross-linking donor peptide sequences (see AAR80345-50 for examples of PPAS proteins). The PPAS proteins ab used as substrates in enzymatic cross-linking reactions catalysed by a transglutanthnase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.
                                                                                      Pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; blocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Protein polymers comprising repeating units and sequences \, - capable of enzyme-catalysed covalent bond formation useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                          Protein polymeric adhesion substrate lysine donor peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                        biocompatible material for wound closure and tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 15; DB 16; Length 7; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conus genus omega-conopeptide group 1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                   (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                      protein polymer adhesive substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 75; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW72631 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                          95WO-US02728
                                                                                                                                                                                                                                                                                       94US-0205518
                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-320413/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA;
                                                                                                                                                                                                                                                       03-MAR-1995;
                                                                                                                                                                                           W09523611-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1999
                             19-APR-1996
                                                                                                                                                                                                                            08-SEP-1995.
                                                                                                                                                                                                                                                                                                                                               Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KGA 3
                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
AAR80377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW72631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic reactions, rheumatoid arthritis, and epilepsy. The present sequence represents a omega-conopeptide group I fragment. Omega-conopeptide components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A method has been developed for the treatment of inflammation in a subject. The method comprises administration of an omega-conopeptide effective to: (i) block voltage-gated calcium channels; (ii) bind with high affinity to an omega-conopeptide binding site; and (iii) inhibit neurotransmitter release from nervous tissue. The method is used to treat inflammation and associated pain. The treatment can also be used to produce analgesia (especially in subjects experiencing neuropathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of inflammation, comprises administration of omega-conopeptide - effective to block voltage-gated calcium channels, bind with high affinity to omega-conopeptide binding site, and inhibit neuro-transmitter release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein polymer; adhesive sealant; wound healing; cross-linking.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 15; DB 19;
100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP, Singh T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 55; 58pp; English.
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/label= Lys, Ser
                                                                                                                                                                                                                                                                                                       91US-0814759.
96US-0675354.
96US-0742774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gohil KC, Justice A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lysine donor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-582596/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (NEUR-) NEUREX CORP.
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic; peptide toxin; opiate; pain; neuronal damage; ischemic condition; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhancing analgesia produced by opiates by administering an omega-conopeptide that inhibits electrically stimulated contraction of guinea pig illum and binds to omega-conopeptide MVIIA binding sites in
                                                                                Gaps
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                                                Length 6;
                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a fragment of an omega-conopeptide.
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB19468-72 represent fragments of omega-conopeptides.
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                                            100.0%; Score 15; DB 21; 100.0%; Pred. No. 7.8e+05;
                                                                                0; Mismatches
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                                                                                                                                                                                                                             AAB19468 standard; peptide; 6 AA.
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98US-0138439.
99US-0298017.
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                                                                                                                                                                                                                                                                                              (first entry)
                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-030946/04.
                                              Query Match
Best Local Similarity
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               6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-1999;
                                                                                                                                                                                                                                                                                              06-MAR-2001
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23-APR-1999
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4 KGA 6
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                                                                                                             1 KGA 3
                                                                                                                                                                                                                                                              AAB19468;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conus sp.
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             Sequence
                                                                              Matches
                                                                                                                                                                                                RESULT 28
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Length 6;

DB 22;

100.0%; Score 15;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector, that encodes one or more segments of a modular polypetide. DNA or DNA libraries produced this way are used to produce modular polypetides, particularly enzymes, which can be used to act on substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vanconycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of a protein encoded by a Streptomyces chrysomallus actinomycin blosynthesis gene which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                               Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the preparation of DNA, in a circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       S chrysomallus actinomycin biosynthase protein acmA fragment #2.
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                                            Indels
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                   Pred. No. 7.8e+05;
Mismatches 0;
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Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 43; 83pp; German.
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100.0%; PI
                                                                                                                                                                                                                                                               AAM47138 standard; Peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2001; 2001WO-DE01578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-2000; 2000DE-1021267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces chrysomallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-049276/06.
N-PSDB; ABA03316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schauwecker F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention.
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4 KGA 6
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3 KGA 5
                                                                                           KGA 3
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                                            Matches
                                                                                                                                                                                                                RESULT 29
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                                                                                                                                                       The invention relates to novel pyrrolobenzodiazepine (PBD) derivatives which are compounds that bind to the minor groove of double stranded mucleic acid sequences, especially at the sequence Purine-Guanine-Purine where Purine is selected from anonine and guanine. The PBD's can be used in combinatorial peptide library screening for binding interactions with nucleic acids. The PBD's can be used in cytotoxic, antibiotic, antiparastitic and antiviral compositions and also in methods of target validation in functional genomics. The peptides AAV83826-Y83833 represent PBD-peptides isolated from a combinatorial peptide library screen on the target nucleic acid sequence
New pyrrolobenzodiazepine derivatives used in the preparation of combinatorial libraries of further pyrrolobenzodiazepine derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; antiparasitic; cytostatic; pyrrolobenzodiazepine;
DNA minor groove; combinatorial peptide library screening; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New pyrrolobenzodiazepine derivatives used in the preparation of combinatorial libraries of further pyrrolobenzodiazepine derivatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYPO-) UNIV PORTSMOUTH HIGHER EDUCATION CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                            Example 8; Page 72; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 72; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY83831 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB02836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-0018730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howard PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-237841/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200012506-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY83831;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ99178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY8383
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The invention relates to novel pyrrolobenzodiazepine (PBD) derivatives which are compounds that bind to the minor groove of double stranded nucleic acid sequences, especially at the sequence Purine-Guanine-Purine

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where Purine is selected from adenine and guanine. The PBD's can be used in combinatorial peptide library screening for binding interactions with nucleic acids. The PBD's can be used in cytocoxic, antibiotic, antibiotic, antiparasitic and antiviral compositions and also in methods of target validation in functional genomics. The peptides AAY838326-Y83833 represent PBD-peptides isolated from a combinatorial peptide library screen on the target nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation. The method comprises measuring a cest compound to treating inflammation. The method comprises measuring the activity of the test compound in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release from nervous tissue. The method is useful for selecting compounds for treating inflammation. The selected compounds are capable of producing analgesia in a mammalian subject with chronic or intractable pain. Nalgesia caused by selected compounds may reduce the reliance on opioid analgesic agents of the prior art which cause dependency and tolerance, requiring potentially dangerous increases in opioid doses to achieve the analgesic effect. The present sequence represents a peptide given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method has been developed of selecting a test compound for treating
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Measuring the activity of test compounds in blocking voltage-gated calcium channels, binding to the omega conopeptide binding site and inhibiting norepinephrine (noradrenaline) release for treating
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin; marine snail; peptide toxin; inflammation; binding; voltage-gated calcium channel; inhibition; norepinephrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gohil KC;
                                                                                                                                                                                                    Length 6;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Singh T, Valentino KL, Miljanich GP,
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                               100.0%; Score 15; DB 21; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  AAY56506 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noradrenaline; anti-inflammatory
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0138439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0742774.
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96US-0675354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0814759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-038270/03.
                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1991;
                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Justice A,
                                                                                                                                                                                                                                                                         1 KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY56506;
                                                                                                                                                                                                                                                                                                            1 KGA
                                                                                                                            AAZ99178
                                                                                                                                                                                                                                     Matches
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98FR-0014470.
                                                                           WPI; 2000-368263/32.
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                   6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
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 18-NOV-1998;
                    18-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2000
                                                                                                                                                                                                                                                                                                                                           1 KGA 3
                                                                                                                                                                                                                                                                                                                                                             4 KGA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY83830;
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                     AAY83830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lysophosphatide acyltransferase; LPAAT; glycerol; rape; fatty acid; 1-acyl-sn-glycerol-3-phosphate acyltransferase; erucic acid; seed oil; triglyceride content; fatty acid composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                     Novel enterocyte growth factors and method for their isolation from intestinal mucosa, useful for treating e.g. cancer -
                                                                                                                                                                                                                                                                               The present sequence is that of inhibiting enterocyte growth factor IEGF17 (mol.wt. 1.15-1.35 kba). The invention provides stimulating and inhibiting enterocyte growth factors (enterocytogenins) (see AAY95755-69) that influence the speed of morphogenesis, either stimulating or inhibiting cell growth. The enterocyte growth factors are nucleopeptides that can be isolated from the intestinal mucosa of warm-blooded animals, such as pigs, rats, dogs etc., using a claimed method of the invention. They can useful for modulating morphogenesis, e.g. in the treatment of cancers, and have higher effectiveness than previous stimulators and inhibitors of cell division.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus sequence of a phosphatide acyltransferase fragment
                                                         'note= "N-terminal guanosine deoxyriboside"
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 15; DB 21; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                              /note= "C-terminal amide"
                                                                                                                                                                                               Roussev GK;
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                Claim 17; Page 38; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93399 standard; Peptide; 6 AA.
  morphogenesis; cancer; therapy
                                                                                                                                                                                               Alexandrov CA, Trifonov BB,
                                                                                                                                     07-FEB-2000; 2000WO-BG00005.
                                                                                                                                                         99BG-0103173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Thes 3; Conservative
                                                                                                                                                                            (TCHO/) TCHOBANOVA A A.
                                                                                                                                                                                                                 WPI; 2000-565282/52.
                                                                                                                                                                                                                                                                                                                                                                                                    6 AA;
                                                                                                40200047605-A2
                                               Modified-site
                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2785911-A1
                                                                                                                                                         12-FEB-1999;
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                                                                                                                  17-AUG-2000
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2 KGA 4
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93399
                    Mammalia
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New nucleic acid encoding lysophosphatide acyltransferase from rape, useful for controlling triglyceride content and fatty acid composition in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a plant lysophosphatide acyltransferase (LPAAT).

1-acyl-sn-glycerol-3-phosphate acyltransferase) polypeptide.

1-acyl-sn-glycerol-3-phosphate acyltransferase) polypeptide.

1-pAAT catalyses acylation of the sn-2 position in glycerol. The polypeptide and polynucleotide are used to regulate activity of LPAAT in plants, specifically rape, particularly to control the fatty acid (especially erucic acid) content of seed oils (used in food and industrial applications). Transformation with LPAAT polynucleotide permits control over triglyceride content and fatty acid composition, allowing these to be adjusted to suit particular applications (especially high erucic acid content for industrial use but low content for food use).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                    Guerche P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; antiparasitic; cytostatic; pyrrolobenzodiazepine;
DNA minor groove; combinatorial peptide library screening; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrrolobenzodiazepine-peptide #5 from combinatorial library screen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a consensus sequence of a fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "conjugated to pyrrolobenzodiazepine group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6;
                                                                                                                                    Barret P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 15; DB 21;
; Pred. No. 7.8e+05;
0; Mismatches 0;
                                                                                                                                    Delseny M, Bourgis F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPO-) UNIV PORTSMOUTH HIGHER EDUCATION CORP.
                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY83830 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 18; 21pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
98FR-0014470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-GB02836
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                                                                                                                                       Renard M, Roscoe TJ,
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gucker-1.rag

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(first entry)
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                                                                                                                                                                                                                                                                                                                                   (TCHO/) TCHOBANOVA A A.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-565282/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
                                                                                                                                                                                                                                   WO200047605-A2
                                                                                                                                                                      Modified-site
                                                                                                                                                                                             Modified-site
                                   07-NOV-2000
                                                                                                                                                                                                                                                                                                           12-FEB-1999;
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                                                                                                                                                                                                                                                           17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
2 KGA 4
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          AAY95765;
                                                                                                                                    Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY95766;
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δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterocyte growth factors and method for their isolation from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of inhibiting enterocyte growth factor ISGF15 (mol.Wt. 1.20-1.40 kba). The invention provides stimulating and inhibiting enterocyte growth factors (enterocytogenins) (see AAY95755-69) that influence the speed of enterocytogenins) (see AAY95755-69) that influence the speed of enterocyte growth factors are nucleopeptides that can be isolated from the intestinal mucosa of warm-blooded animals, such as pigs, rats, dogs etc., using a claimed method of the invention. They cancers, and have higher effectiveness than previous stimulators and inhibitors of cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                          IEGF15; inhibiting enterocyte growth factor: enterocytogenin; nucleopeptide; proliferative; antiproliferative; antitumour; morphogenesis; cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 21; Length 6; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intestinal mucosa, useful for treating e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                             /note= "N-terminal adenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                     Inhibiting enterocyte growth factor IEGF15
                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexandrov CA, Trifonov BB, Roussev GK;
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 38; 48pp; English.
                                                                                          AAY95764 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY95765 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2000; 2000WO-BG00005
                                                                                                                                                                                                                                                                                                                                                                                                                    99BG-0103173
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             (TCHO/) TCHOBANOVA A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-565282/52
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                                                                                                                                                                                                                                                                                                                                            WO200047605-A2
                                                                                                                                                                                                                                                                               Modifled-site
                                                                                                                                                                                                                                                                                                        Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1999;
                                                                                                                                            07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000
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2 KGA 4
       1 KGA 3
                               4 KGA 6
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                                                                                                                   AAY95764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                             Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
AAY95765
ID AAY95
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of inhibiting enterocyte growth factor IEGF16 (mol.wt. 1.10-1.30 kDa). The invention provides stimulating and inhibiting enterocyte growth factors (enterocytogenins) (see AAY95755-69) that influence the speed of morphogenesis, either stimulating or inhibiting cell growth. The enterocyte growth factors are nucleopeptides that can be isolated from the intestinal mucosa of warm-blooded animals, such as pigs, rats, dogs etc., using a claimed method of the invention. They care useful for modulating morphogenesis, e.g. in the treatment of cancers, and have higher effectiveness than previous stimulators and inhibitors of cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                            IEGF16; inhibiting enterocyte growth factor; enterocytogenin; nucleopeptide; proliferative; antiproliferative; antitumour; morphogenesis; cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEGF17; inhibiting enterocyte growth factor; enterocytogenin; nucleopeptide; proliferative; antiproliferative; antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 15; DB 21; Length 6; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-terminal guanosine"
Inhibiting enterocyte growth factor IEGF16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting enterocyte growth factor IEGF17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roussev GK;
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Page 38; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alexandrov CA, Trifonov BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2000; 2000WO-BG00005.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CART; cocaine and amphetamine regulated transcript; rat; anorectic; appetite regulator; treatment; obesity; type II diabetes; bulimia; autoimmune disease; inflammation; arthritis; type I diabetes; menopause; multiple sclerosis; stroke; osteoporosis; Parkinson's disease; adipsia; menstrual complication; cancer.
                                                                       group 1 and 2. Omega-conopeptides are components of peptide toxins produced by marine snails of the genus Conus, and which act as calcium channel blockers. The invention relates to a method of producing analgesia in a mammal that comprises administering an omega conopeptide having activities in (a) inhibiting electrically stimulated contraction of guinea pig ileum and (b) selectively binding to omega conopeptide WVIRA binding sites in neuronal tissue, where these activities are within the ranges of those of omega-conoctosins WIIIA and TVIA. The method is used for treating chronic pain, especially neuropathic pain.
                                                       Sequences AAW95590-594 represent fragmnets within omega-conopeptides
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated cocaine and amphetamine regulated transcript proteins - with anorectic and adipsic activity, useful for regulating appetite, particularly for treating obesity, also related nucleic acid,
                                                                                                                                                                                                                                                                                                                                                   ó,
                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Judge ME, Kristensen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat CART (62-102) protease digestion fragment #2.
                                                                                                                                                                                                                                                                                                              100.0%; Score 15; DB 20; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors, transgenic organisms and antibodies
                                                                                                                                                                                                                                                                                                                                 Pred. No. 7.8
0; Mismatches
                Disclosure; Column 17; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Page 37; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW90100 standard; Protein; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christiansen K, Hastrup S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-DK00128
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97DK-0000358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                            Query Match 100.

Best Local Similarity 100.

Matches 3; Conservative
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                                                                                                                                                                                                                                                                            6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        1 KGA 3
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW90100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / of test compound in blocking voltage-gated calcium channels,
to omega conopeptide binding site and inhibiting norepinephrine
osteoporosis, menopausal symptoms, menstrual complications and Parkinson's disease. CART is the protein responsible for the anorectic and adipsic phenotype associated with certain cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marine snail; omega-conopeptide; calcium channel blocker; toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic; norepinephrine release inhibitor; schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation; epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Selecting a compound for producing analgesia involves measuring activity of test compound in blocking voltage-gated calcium characteristy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a fragment of an omega-conopeptide.
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                                                                                                                                                                 Length
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                                                                                                                                                              100.0%; Score 15; DB 20;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 15; DB 21;
100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB14373 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conopeptide group 1 fragment #1.
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93US-0049794.
96US-0675354.
98US-0138439.
91US-0814759.
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Les 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELAN-) ELAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gohil KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-490177/43
                                                                                                                                                                                       Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AA;
                                                                                                                6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1993;
03-JUL-1996;
21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB14373;
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                                                                                                                Sequence
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                                                                                                                                                                    Query Match
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Brunner H, Kapurniotu A;

97DE-1025619 97DE-1025619

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Peptides containing amino acid sequence {\tt GA} - useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of
                                                                                                                                                                                                                                                                        (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Column 5; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type II diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-121938/11
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                         DE19725619-A1
                                                                                                                                                                                                                                                                                                                                    Bernhagen J,
                                                                                                                                               17-JUN-1997;
                                                                                                                                                                                                           17-JUN-1997;
                                                                                     24-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is a cyclic peptide which competes with and competitively inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR). This is a low affinity nerve growth factor (MGF) receptor which is expressed by melancoytes and keratinocytes of the basal epidermis. Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2 protein. If the receptor is occupied by appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other examples of appropriate ligands include this cyclic peptide. This peptide is based on the sequence of the binding fragment of beta-amyloid, which binds to p75NTR in Alzheimer's disease. This cyclic peptide can be used in methods involve using this peptide or peptides AAY39233-Y39234 to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting apoptosis. The new method can induce or maintain hair growth, hair colour or skin colour. Inducing or maintaining hair growth is useful for treating alopecia areata or male pattern baldness in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                     /note= "N-terminus is attached via a peptide bond to the C-terminus amino acid at position 6\,^{\circ}
                                                                                                                                                                                                                                        to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Controlling or manipulating melanocyte and keratinocyte cell death,
                                                                                                                                                                                                                                 "C-terminus is attached via a peptide bond the N-terminus amino acid at position 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating, e.g. alopecia areata
                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 40; 67pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eller M, Gilchrest BA,
                                                                                                                                                                                              6
/note= '
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Best Local Similarity
                                                                                                         Modified-site
                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                              WO9939728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1999;
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                      Synthetic
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are useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of type II diabetes mellitus, Alzheimer's disease and spongiform encephalopathies (e.g. CJD, scrapie and BSE).
This invention describes novel agonists (competitive inhibitor) and/or inhibitors of amyloid formation peptides which are 3-15 amino acids in length and contain at least the active sequence GA. The new peptides
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omega-conopeptide; peptide toxin; snail; calcium channel blocker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valentino KL;
                                                                                                                                                                                                                      Length 6;
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                                                                                                                                                                                          100.0%; Score 15; DB 20; ilarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Migmatal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW95590 standard; protein; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conopeptide group 1 fragment.
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91US-0814759.
96US-0675354.
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                                                                                                                                                                                     Query Match
Best Local Similarity
Best Local 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-120002/10.
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                                                                                                                                                                         AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1991;
03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS5859186-A
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A hexapeptide sequence present in the gamma chain of native fibrinogen (see AAR39599) was mutated by the single substitution of a glycine for glutamine to produce KGAGDV (AAR39597). The novel peptide was found to retain Leukocyte Response Integrin ligand binding and PMN activation. Antibodies to the betal and beta2 integrin families had no effect on KGAGDV binding to LRI; antibodies to both beta3 and Integrin-Associated Protein inhibited KGAGDV binding to LRI.
                                                 A novel peptide comprising at least four residues from the contiguous amino acid sequence shown, is capable of binding endothelin or its precursor. The peptide is useful for determining the presence of endothelin and as an agent for preventing or inhibiting the action of endothelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRI; beta-integrin; cytoadhesin; ligand-binding specificity; polymorphonuclear neutrophil; integrin associated protein; IAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide of lysine glycine alanine glycine aspartic acid valine amino acid chain - comprises ligand for leukocyte response integrin, inhibiting fibrinogen-dependent activation of polymorphonuclear neutrophil
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                                                                                                                                                                                              Length 6;
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100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Leukocyte Response Integrin ligand peptide.
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                                                                                                                                                                                                                                                                                                                                                           AA.
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                           Claim 1; Page 1; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                        AAR39597 standard; peptide; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-0866678.
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                                                                                                                                                                                                                          Conservative
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endothelin function
                                                                                                                                                                                                         Local Similarity
nes 3; Conserv
                                                                                                                                                                  6 AA;
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                                                                                                                                                                                                                                                                      1 KGA 3
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                                                                                                                                                                                                                                                                                                                                                                                     AAR39597;
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Matches
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Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor; NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid; Alzheimer's disease; pseudo-ligand; hair growth; hair colour; skin colour; alopecia areata; male pattern baldness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claimed monoclonal antibodies recognise an epitope in the first domain of a N.meningitidis strain IM2169- or IM2394-related transferrin Tbp2 subunit homologous to one of the epitope sequences YKGTW, EFEVDFSDKTIKGTL, EGGFYGPKGEEL or AVFGAK (AAR88663-R88666) from N.meningitidis strain IM2394 and cannot recognise an epitope in the third domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor \ensuremath{\mathsf{Tbp2}}
                                                                                                                                                                  N.meningitidis IM2394 transferrin receptor Tbp2 domain 1 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                            Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine; passive immunisation; immunotherapy; monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclic peptide used to inhibit p75-NTR mediated apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          (INMR ) PASTEUR MERIEUX SERUMS & VACCINS. (TRGE ) TRANSGENE SA.
                                                                                                                                                                                                                                      Neisseria meningitidis (strain IM2394).
                                                                                                                                                                                                                                                                                                                                                                                                                   Mazarin V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY39235 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 50; Page 96; 114pp; French.
                                                                                 AAR88666 standard; Protein; 6 AA.
                                                                                                                                                                                                                                                                                                                     95WO-FR00701
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                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Legrain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-030562/03.
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Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA;
                                                                                                                                                                                                                                                                                                                                                31-MAY-1994;
                                                                                                                                                                                                                                                                                                                     30-MAY-1995;
                                                                                                                                        30-AUG-1996
                                                                                                                                                                                                                                                                WO9533049-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs E, 1
Millet MBJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KGA 5
1 KGA 3
                                                                                                            AAR88666;
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                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic; Alzheimer's disease; neurotrophin receptor; NTR; human; cyclic.
                                                                                                                                                                                                                                                                  Inhibition of beta-amyloid binding to the p75 nerve growth factor receptor using polypeptides, useful in the diagnosis and treatment of e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
result of the bonding between the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-amyloid p75NTR binding inhibiting cyclic pentapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 15; DB 22; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "disulphide bridge"
               cysteine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       Claim 2; Column 21; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB07972 standard; peptide; 5 AA.
                                                                                                                                    96US-0625765
97WO-US04966
                                                                                                       98US-0163095
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                                                                                                                                                                                                               Gilchrest BA, Yaar M;
                                                                                                                                                                                  (UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                             WPI; 2001-380482/40.
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Best Local Similarity
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                                                                                                                                    29-MAR-1996;
                                                                                                       29-SEP-1998;
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                                                                           05-JUN-2001
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the p75 nerve growth factor receptor (NGFR) of a cell. The method involves contacting the cell with a substance having the amino acid agequence lysine-glycine-lysine or lysine-glycine-alanine. The substance binds to the p75 NGFR resulting in the inhibition of beta-amyloid peptide binding to the p75 NGFR. The invention is useful or beta-amyloid peptide binding to the p75 NGFR. The invention is useful for evaluating the risk of an individual to develop Alzhaimer's disease and methods of therapy for Alzhaimer's disease using peptides that bind to the neurotrophin receptor. (NTR) and competitively inhibit the binding of beta-amyloid to the receptor. In vitro methods are also provided for screening substances and identifying those capable of inhibiting, or decreasing cell apoptosis mediated by beta-amyloid. The present sequence represents a cyclic pentapeptide that competes for p75NTR binding with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of inhibiting beta-amyloid binding to
                                                                                                                                                                                                                                                                                                                                                Evaluating risk of an individual to develop Alzheimer's disease using cultured neural crest-derived melanocytes and methods of therapy for Alzheimer's disease using peptides that bind to the neurotrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 15; DB 23; ilarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR34869 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 8; 19pp; English.
                                                        98US-0163095.
96US-0625765.
97WO-US04966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91JP-0232991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91JP-0232991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HITB ) HITACHI CHEM CO LID
29-MAY-2001; 2001US-0866898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endothelin binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the beta-amyloid peptide.
                                                                                                                                                                                                                                        Yaar M;
                                                                                                                                                                                                                                                                                                 WPI; 2002-443695/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-140359/17.
                                                                                                                                                                         (UYBO-) UNIV BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA;
                                                                                                                                                                                                                                     Gilchrest BA,
                                                        29-SEP-1998;
29-MAR-1996;
28-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP05078391-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KGA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR34869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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5 AA;
   (FUJI/) FUJII T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                        at C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            1 KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KGA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG64003;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                        dronb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG64003
    δ
                                                                                                                                                                                                                                                                                                                                                                                          0
                                                           Agonist; cytotoxic; competitive inhibitor; amyloid formation; treatment; type II diabetes mellitus; Alzheimer's disease; CJD; scrapie; BSE; spongiform encephalopathy.
                                                                                                                                                                                                                                                                                       This invention describes novel agonists (competitive inhibitor) and/or inhibitors of amyloid formation peptides which are 3-15 amino acids in length and contain at least the active sequence GA. The new peptides are useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of type II diabetes mellitus, Alzheimer's disease and spongiform encephalopathies (e.g. CJD, scrapie and BSE).
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                     Peptides containing amino acid sequence GA - useful for inhibiting amyloid formation and associated cytotoxicity in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 15; DB 20; Length 5; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-HIV; vaccine; gp120; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-HIV peptide with affinitiy to gp120 number 72.
                                                                                                                                                                                   (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                    Bernhagen J, Brunner H, Kapurniotu A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM51322 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                       Claim 5; Column 5; 8pp; German.
                                                                                                                                                  97DE-1025619
                                                                                                                                                                   97DE-1025619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-2000; 2000JP-0006182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2000; 2000JP-0006182
                         18-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                       type II diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.

Best Local Similarity 100.

Matches 3; Conservative
                                          DE19725619 peptide #9
                                                                                                                                                                                                                      WPI; 1999-121938/11.
                                                                                                                                                                                                                                                                                                                                                      5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2001192399-A.
                                                                                                                DE19725619-A1.
                                                                                                                                                  17-JUN-1997;
                                                                                                                                                                  17-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                 24-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   1 KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                        1 KGA 3
                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
        AAW93018;
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM51322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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The peptides are useful in the treatment of HIV and in the preparation of a HIV vaccine.
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to peptides (AAM51251-AAM51381) with a higher affinity to gp120, part of the outer shell of HIV, than known peptides. Peptides with affinity to gp120 shown by formula (H-)A1-A2-A3-A4-A5-R (1), A1-A2-A3-A4-A5-R (2) or H-A1-A2-A3-A4-A5-R (2) or H-A1-A2-A3-A4-A5-R (6).

A1 - A2P, A3-A4-A5'-R (3), (H-)a1-a2-a3-a4-a5'-R (6).

A1 - A3P, L9s, Val, Glu, Glu, Gly, Asn or Tyr residue;

A2 - Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr residue;

A3 - Lys, Val, Asp, Arg, Ala or Trp residue;

A4 - A1a, Trp or Gly residue;

A5 - Gly, Val, Leu, Leu, Carlo, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His, Lys, Arg, Phe, Tyr or Trp residue;
al' = Tyr, Arg, Phe, Gly, Trp, His or Asp residue, or a polypeptide residue having optional amino acids at N-terminal; and as = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His, Lys, Arg, Phe, Tyr or Trp, or a polypeptide residue having optional amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Al' = Asp, Lys, Val, Glu, Gly, Asn or Tyr residue, or a polypeptide residue having optional amino acids at N-terminal;
A5' = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His, Lys, Arg, Phe, Trp, Pro or Tyr residue, or a polypeptide residue having optional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acids at C-terminal;
al = Tyr, Arg, Phe, Gly, Trp, His or Asp residue;
a2 = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys residue;
a3 = Lys, Tyr, Arg, Glu, Met or Trp residue;
a4 = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asp, Gln, His, Lys, Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                      Novel peptides with affinity to gp 120, useful for treatment of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; beta-amyloid; nootropic; neuroprotective; anticonvulsant; p75 nerve growth factor receptor; inhibitor; Alzheimer's disease; neurodegenerative disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "the peptide has a cyclic structure as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta-amyloid-derived cyclic peptide #1.
                                                                                                                                                                                                                                                                            Example 2; Page 10; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG64003 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 3; Conservative
WPI; 2001-605354/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phe or Trp residue;
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AAY39238 standard; peptide; 5 AA

RESULT 8 AAY39238

|||| 2 KGA 4

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1 KGA 3

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                                                                                                diseases, neuropathies, immunodeficiencies, geriatric disease, transplant rejection diseases, hyperproliferative diseases, autoimmune diseases and
cellular condition achievable by application of staurosporine, and diseases responsive to inhibition of a cellular condition achievable by application of staurosporine. The diseases include neurodegenerative
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage site between the leader sequence and VP4 of clone pRMC35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - which lacks an
                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                  Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  live recombinant foot-and-mouth disease virus; FMD virus; active leader proteinase protein; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initiation codons; Lab; leader sequence; Lb;
live recombinant foot-and-mouth disease virus; FMD
                                                                                                                                                                                                                                                                                        100.0%; Score 15; DB 19;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mason PW, Piccone ME, Rieder E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Flg 1b; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW80207 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0653037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .mmunisation against FMD
                                                                                                                                                                   dermatological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USDA ) US SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-582501/49.
                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV66361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grubman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5824316-A
                                                                                                                                                                                                                                                                                                                                                                                                                       KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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This sequence is used in the production of a cyclic peptide AAY39235.

The cyclic peptide competes with and competitively inhibits beta-amyloid
binding to the p75 neurotrophin receptor (p75NRR). P75NRR is a low
affinity nerve growth factor (NGF) receptor which is expressed by
affinity nerve growth factor (NGF) receptor which is expressed by
melanocytes and keratinocytes of the basal epidermis. Apoptosis can be
inhibited by p75NTR via the upregulation of the BCl-2 protein. If the
receptor is occupied by appropriate ligands e.g. neurotrophins,
apoptosis is inhibited. Other examples of appropriate ligands include
this cyclic peptide. This peptide is based on the sequence of the binding
this cyclic peptide can be used in methods to p75NTR in Alzheimer's disease.
This cyclic peptide can be used in methods to control or manipulate
keratinocyte or melanocyte cell death. The methods involve using this
peptide or peptides AAY39234-Y39235 to bind as a pseudo-ligand to the p75
neurotrophin receptor, inhibiting apoptosis. The new method can induce or
maintain hair growth, hair colour or skin colour. Inducing or maintaining
hair growth is useful for treating alopecia areata or male pattern
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0
                                                                                                                          p75NTR; p75 neurotrophin receptor; nerve growth factor;
NGF; melanocyte; keratinocyte; apoptosis; Bc1-2; Alzheiner's disease;
NSeudo-ligand; hair growth; hair colour; skin colour; alopecia areata;
male pattern baldness.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Controlling or manipulating melanocyte and keratinocyte cell death, useful for treating, e.g. alopecia areata
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                                                                                       Peptide used for the generation of p75NTR binding peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Yaar M;
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baldness in vertebrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilchrest BA,
                                                                                                                                                                                                                                                                                                                                                                                                          (UYBO-) UNIV BOSTON.
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Matches 3; Conserv
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2 KGA 4
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AAW93018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW73300;
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       \mathbf{x} \otimes \mathbf{x} \otimes \mathbf{y} \otimes 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptide is capable of binding endothelin or its precursor. The peptide is useful for determining the presence of endothelin and as an agent for preventing or inhibiting the action of endothelin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment; neurotrophin receptor p75; p75NTR; nerve growth factor; NGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endothelin-binding peptide comprising 4 or more aminoacid(s) useful for detecting endothelin and modifying or inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
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/note= "Optional disulphide bond"
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                                                                                                                                                                                                            91JP-0232991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR34869-80
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nes 3; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelin function
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                                                                                                                                         30-MAR-1993
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   Synthetic.
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                                                                      The invention relates to methods of therapy for Alzheimer's disease using peptides (AAW45343-6) that bind to the neurotrophin receptor p75 nerve growth factor receptor (NGFR) and competitively inhibit the binding of a beta-amyloid to the p75 NGFR. Also described is a new method for evaluating the risk of an individual to develop Alzheimer's disease using cultured neural crest-derived melanocytes. The methods can be used for diagnosing and treating Alzheimer's disease and other neurodegenerative diseases mediated by beta-amyloid protein, or by aberrant activation of the low affinity NGFR localised on neural cell surfaces, such as autoimmune encephalomyelitis, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a fragment of a polypeptide of the invention. The polypeptides were isolated from the HL60 cell line. The polypeptide can be used as a drug, or as marker or surrogate marker for monitoring a cellular condition or disease achievable by application of staurosporine. They can also be used for identification of a drug for treatment of a disease selected from disease responsive to induction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HL60; human; staurosporine; neurodegenerative disease; neuropathy; immunodeficiency; geriatric disease; transplant rejection; therapy; hyperproliferative disease; autoimmune disease; dermatological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cortico-basal degeneration, progressive supra nuclear palsy, Gerotman-Shaussless Scheinker syndrome, Neimann-Pick disease, and progressive supranuclear palsy. In the diagnostic tests, the human melanocytes, which are easily obtainable from skin biopsies, are good model cells for the study and diagnosis of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 7.8e+05;
Live 0; Mismatches 0; Indels
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Disclosure; Page 21; 42pp; English.
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Best Local Similarity
The 3; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes substituted cholic acid based scaffold molecules, prepared by solid phase synthesis. The substituted cholic acids are prepared by initial solution synthesis of a scaffold folding amino acids with 3 orthogonal protecting groups. Subsequent solid phase synthesis provides build up of the target molecules, either as discretes or in mixture. The molecules may then be screened on the resin or cleaved from the resin and then screened in solution. The molecules are potential mimetics of larger peptides. The present sequence represents a single compound of the invention.
The peptide is useful for determining the presence of endothelin and as an agent for preventing or inhibiting the action of endothelin. See also AAR34869-80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cholic acid based scaffolds for multidimensional presentation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Substituted cholic acid; scaffold molecule; solid phase synthesis;
                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 15; DB 20; Length 4; 11arity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                             Length 4;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single compound for use in a scaffolded library.
                                                                                                                             100.0%; Score 15; DB 14; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 23; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                             AAY23842 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-DK00547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0068073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-405023/34.
                                                                                                                               Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AA;
                                                                                           4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoeg-Jensen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9931124-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-1997;
12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-1999
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                                                                                                                                                                                                                1 KGA 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                        AAY23842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mimetic.
                                                                                                                                                                                                                                                                                                                      RESULT 2
AAY23842
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AAE03421
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The present invention relates to an antisense compound comprising nucleotides complementary to a nucleic acid sequence coding for anyloid precursor protein (APP) and which inhibits the expression of amyloid beta protein (Abeta) portion of APP coding sequence while permitting the expression of at least a portion of APP polynucleotide 5' to the Abeta portion of APP coding sequence. This antisense compound is useful for modulating the expression of Abeta in cells or tissues, for preventing or treating a disease or condition associated with expression of Abeta, in particular Albreimer's disease. The antisense compound is also useful for improving cognitive ability in a mammal having a disease or condition associated with the expression of Abeta.
                                                                                                                                                                                                                                               Human; antisense; amyloid precursor protein; APP; amyloid beta protein; AbetaP; Alzheimer's disease; cognitive ability; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antisense compounds for modulating expression of amyloid beta protein in cells or tissues and for preventing, treating conditions associated with expression of amyloid beta protein, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are used in antisense therapy. The present sequence is a peptide encoded by human antisense oligonucleotide OL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                    Peptide encoded by human antisense oligonucleotide OL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Precursor; pre endothelin; agent; inhibitor; synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 68; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR34877 standard; peptide; 5 AA.
AAE03421 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000; 2000WO-US33383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0458481
                                                                                                                                                                                                                                                                                       AbetaP; Alzheimer's disease
nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endothelin binding peptide
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYSL-) UNIV SAINT LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-381626/40.
N-PSDB; AAD07948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200142266-A1
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-1993
                                                                                                                            06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-2001
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Page 1

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2002, 14:03:49; Search time 34 Seconds (without alignments) 11.757 Million cell updates/sec November Run on:

GUCKER-1 15 Title:

1 kga 3 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched:

430 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 3 Maximum DB seq length: 20

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Database :

SIDS2/ggdata/geneseq_geneseqp_embl_AA1989_DAT:*

SIDS2/ggdata/geneseq_geneseqp_embl_AA1989_DAT:*

SIDS2/gcgdata/geneseq_geneseqp_embl_AA1990_DAT:*

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/SIDSZ/gcgdata/geneseqg/geneseqgp.embl/AA1987.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* A_Geneseq_101002:* 14: 15: 16: 17: 18: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | Endothelin binding | Single compound fo | Peptide encoded by | Endothelin binding | Peptide used for d | HL60 cell line pro | Cleavage site betw | Peptide used for t | DE19725619 peptide | Anti-HIV peptide w |
|---|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | ID | AAR34871 | AAY23842 | AAE03421 | AAR34877 | AAW45345 | AAW73300 | AAW80207 | AAY39238 | AAW93018 | AAM51322 |
| |
B | 14 | 20 | 22 | 14 | 18 | 19 | 19 | 20 | 20 | 22 |
| | Query
Match Length DB | 4 | 4 | 4 | 5 | 2 | Ŋ | S | 5 | 5 | ß |
| æ | Query
Match 1 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| | Score | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 |
| | Result
No. | 1 | 7 | m | 4 | ស | 9 | 7 | ω | 6 | 10 |

| Human beta-amyloid
Beta-amyloid p75NT | Endothelin binding | Res | git | Cyclic peptide use | DE19725619 peptide | lde | 9 | Conopeptide group | | Inhibiting enteroc | Inhibiting enteroc | Consensus sequence | Pyrrolobenzodiazep | Pyrrolobenzodiazep | Peptide SEQ ID NO: | id. | S chrysomallus act | Protein polymeric | Conus genus omega- | н | 5619 pe | S chrysomallus act | | PM-1/BSA peptide. | | BSA | /BSA | HIV-1 group 0 stra | Beta-amyloid fragm | | Beta-amyloid fragm | 9 pe | C) |
|------------------------------------------|--------------------|---------|-------|--------------------|--------------------|------|---------|-------------------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------|--------------------|-------------------|--------------------|---------|---------|--------------------|---------|-------------------|------|---------|---------|--------------------|--------------------|---------|--------------------|---------|---------|
| 2 AAG64003
3 ABB07972 | AAR3486 | AAR3959 | AAR88 | AAY3923 | 0 AAW93019 | | AAW9010 | | AAY9576 | AAY9576 | AAY9576 | AAY933 | AAY83 | AAY83 | AAY56 | AAB19 | AAM47 | | AAW72 | AAW4976 | AAW9302 | AAM4714 | AAM4714 | AAR3728 | | AAR3728 | AAR3728 | 7 AAW07226 | AAW453 | AAW5753 | AAY3923 | AAW9302 | AAW9302 |
| 5 22 23 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5 100.0 | | 100. | | 5 100.0 | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | 100. | H | 100. | 100. | 100. | 100.0 |
| ää | ij | 15 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 15 | |
| 11 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 38 | 40 | 41 | 42 | | 44 | |

ALIGNMENTS

AAR34871 standard; peptide; 4 AA. Endothelin binding peptide. 18-AUG-1993 (first entry) AAR34871; RESULT 1 AAR3487.

Precursor; pre endothelin; agent; inhibitor; synthetic.

Synthetic.

JP05078391-A.

30-MAR-1993.

91JP-0232991. 12-SEP-1991; 91JP-0232991. 12-SEP-1991; (HITB) HITACHI CHEM CO LID.

WPI; 1993-140359/17.

Endothelin-binding peptide comprising 4 or more aminoacid(s) useful for detecting endothelin and modifying or inhibiting endothelin function

Example; Page 5; 8pp; Japanese.

The peptide is capable of binding endothelin or its precursor.

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Matches
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                   OTHER INFORMATION: Description of Artificial Sequence: sequence from CTHER INFORMATION: a phage display peptide library US-08-925-002-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09001984C
Fatent No. 624531
GENERAL INFORMATION:
APPLICANT: Laal, Suman
APPLICANT: Laal, Suman
APPLICANT: Laal, Suman
APPLICANT: Belisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-011
CURRENT FILING DATE: 1997-12-31
PRIOR FILING DATE: 1997-12-31
PRIOR FILING DATE: 1966-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 10
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                                                                                                                                                           100.0%; Score 15; DB 3; Length 10; ilarity 100.0%; Pred. No. 2.5e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Glichrest, Barbara A.
APPLICANT: Yaar, Mina
TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: ALGHEIMER'S DISEASE
TILE REFERENCE: BU96-09A2
CURRENT PAPLICATION NUMBER: US/09/163,095
CURRENT FILING DATE: 1998-09-29
EARLIER APPLICATION NUMBER: PCT/US97/04966
EARLIER APPLICATION NUMBER: PGT/US97/04966
EARLIER PILING DATE: 1997-03-28
EARLIER FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4
LENGTH: 10
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-13
                                                                                                                                                                                                                                                                                                                                                                RESULT 43
US-005-163-095-4
Sequence 4, Application US/09163095
; Patent No. 6242416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Cyclic peptide US-09-163-095-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                 Best_Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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| KGA 8
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                                                                                                                                                              Query Match
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CURRENT FILING DATE: 1998-06-12
EARLIER FILING DATE: 1997-06-17
SOFTWARE: PatentIn Ver. 2.1
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                             Length 10;
                                                                             0; Indels
                     100.0%; Score 15; DB 4; I
100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 9, 2002, 14:13:48 Job time: 15 secs
                                                                                                                                                                                                                                                                                                    ; Sequence 14, Application US/09097194 ; Patent No. 6359112
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kapurniotu, Afroditi
APPLICANT: Bernhagen, Juergen
Query Match
Best Local Similarity 100.0
Thes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-097-194-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  RESULT 45
US-09-097-194-14
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| KGA 8
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LENGTH: 10
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA Binding peptides and Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALLIDE
COMPUTER: IBM COMPALLIDE
COMPUTER: IBM COMPALLIDE
COMPUTER: TOWNER: USON VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USON-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-AUG-1993
ATTONER; OS-MAR-1993
ATTONER; MARE: USON-1993
TELEPHONE: (415) 576-0200
100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                               Sequence 835, Application US/08159339A Patent No. 6037135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Grete, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 835:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 3; Conservative
                             Conservative
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MOLECULE TYPE: peptide
Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                              RESULT 40
US-08-159-339A-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-159-339A-835
                                                                           1 KGA 3
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Sequence 846, Application US/08159339A Patent No. 6037135

RESULT 41 US-08-159-339A-846

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APPLICANT: Granoff, Dan M.
APPLICANT: Granoff, Dan M.
APPLICANT: Moe, Gregory R.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 1238.002
CURRENT APPLICATION NUMBER: US/08/925,002
CURRENT FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATCHLIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                         APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Calls, Esteban
TITLE OF INVENTION: HIA Binding peptides and Their
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 15; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                 NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORENATION SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-NAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISKATION NUMBER: 32,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/08925002; Patent No. 6048527; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 846:
                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                    Kubo, Ralph T.
Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-159-339A-846
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-925-002-40
                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 KGA 9
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Query Match
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Patent No. 5942415

GENERAL INFORMATION:
APPLICANT: Schraven, B. et al.
TITLE OF INVERTION: SKAP55 Compositions and Methods of Use Therefor NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 15; DB 2; Length 10
100.0%; Pred. No. 2.5e+02;
Live 0; Mismatches 0; Indels
                                                                                           STATE: CALLIVONALA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOUTER: IBM PC COMPATIBLE
COMPOUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: 39,787
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 39,787
REGISTRATION NUMBER: 39,787
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2402
TELEPHONE: RAIS) 326-2422
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
TENGTHERY: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TEADABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: BACENTING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,636
FILING DATE: 13-APR-1994
CLASSIFICATION: 530
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BBI-066
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APPLICATION NUMBER: US
FILING DATE: Herewith
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-(TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0
Best Local Similarity 100.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-08-633-148-13
                                                                 SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Gelis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        100.0%; Score 15; DB 2; L ilarity 100.0%; Pred. No. 2.5e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 794, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 794:
TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-159-339A-794
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 39
US-08-159-339A-794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
                                                                                                                                                                                                                                                                                            1 KGA 3
                                                                                                                                                                   US-08-713-636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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Length 10;

100.0%; Score 15; DB 3;

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GENERAL INFORMATION:
APPLICANT: MORIOKA, SHINJI
APPLICANT: USKI, JUN
TITLE OF INVENTION: CONTAINING THE SAME AND METHOD FOR EXPRESSING FOREIGN
TITLE OF INVENTION: GONES USING THE SAME
TITLE OF INVENTION: GONES USING THE SAME
OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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TITLE OF INVENTION: 29 Human Secreted Proteins FILE REFERENCE: PZ015P1
                                     CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/1709
EARLIER FILING DATE: 1998-08-29
EARLIER FILING DATE: 1997-08-29
MUMBER OF SEQ. ID NOS: 128
NUMBER OF SEQ. ID NOS: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-221P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08750007
Patent No. 5801016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.
Matches 3; Conservative
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ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-257-179-112
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 112
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
TITLE OF SEQUENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSE: TWO BEBARCADERO & TOWNSENT & CREW LLP
STREET: TWO BEBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23
                                                                       Gaps
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                     100.0%; Score 15; DB 1; Length 10; ilarity 100.0%; Pred. No. 2.5e+02; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 396-2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/633,148 FILING DATE: 16-APR-1996 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08633148; Patent No. 5864018; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/08633148 ; Patent No. 5864018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
Ouery Match
Best Local Similarity
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STRANDEDNESS: si
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Best Local Similarity
Matches 3; Conserv
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3 KGA 5
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US-08-633-148-13
                                                                                                                1 KGA 3
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US-08-633-148-5
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; OTHER INFORMATION: Description of Artificial Sequence: manufactured
; OTHER INFORMATION: by BACHEM
US-09-202-832-8
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APPLICANT: IZU, YUKIKO
APPLICANT: TANKAA, TELSUKI
APPLICANT: TANKAA, TELSUKI
APPLICANT: TANKAA, TELSUKI
APPLICANT: TANIGAWA, TECSUO
APPLICANT: TANIGAWA, TECSUO
APPLICANT: TSUNASARA, SUSSUMU
APPLICANT: KATO, IKUNOSHIN
TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
FILE REFERENCE: 1422-368P
CURRENT APPLICATION NUMBER: US/09/202,832
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATCHIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
100.0%; Score 15; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 15; DB 3; I
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,586
FILLING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 112, Application US/09257179; Patent No. 6410709
                                                                    ATTORNEY AGENT INFORMATION:
NAME: OSter, Jeffrey B.
REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: 02036
TELEPHONE: 516 562 9404
TELEPHONE: 516 562 9404
INFORMATION FOR SEC ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09202832
Patent No. 6194190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                         SS: single
unknown
                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-586-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 3; Conserv
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US-09-257-179-112
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APPLICANT: Bucala, Richard J. et al.
TITLE OF INVENTION: Inhibition of Migration Inhibitory Factor in the Treatment of
TITLE OF INVENTION: Cytokine-Mediated Toxicity
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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HLA Binding peptides and Their
Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 15; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0;
                                NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08471586 Patent No. 6080407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 817:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 Community Drive
                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: anino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP: 11030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 350 CommCITY: Manhasset
STATE: New York
                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KGA 3
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                                                                                                                                Length 9;
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                            100.0%; Score 15; DB 3; L
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: TASTEM: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/027,746
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: US-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: US-MAR-1993
APPLICATION NUMBER: US-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEBDISTRATION NUMBER: S2,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                 US-08-159-339A-792;
Sequence 792, Application US/08159339A
Parent No. 6037135;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                         ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-546-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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Matches 3; Conserva
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TYPE: amino acid
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                    STRANDEDNESS:
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3 KGA 5
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                                                                                                                                                         TITLE OF INVENTION: His Binding peptides and Their TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 15; DB 3; I Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUBBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 817, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
Sequence 805, Application US/08159339A Patent No. 6037135
                                           GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 805:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-159-339A-805
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-159-339A-817
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Best Local Similarity 100. Matches 3; Conservative

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RESULT 28
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                                                                                                                                                              APPLICANT: Brunner, Herwig Title De Turbinitors of Amyloid TITLE OF INVENTION: Peptides Used As Agonists And/or Inhibitors of Amyloid TITLE OF INVENTION: Peptides Used As Agonists And Also For Use In TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And TITLE OF INVENTION: In Spongiform Encephalophathies
FILE REPERENCE: US 09/097,194
CURRENT APPLICATION NUMBER: US/09/097,194
CURRENT FILING DATE: 1998-06-12
EARLIER APPLICATION NUMBER: DE 197 25 619.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEPLICANT: CLANEL, FRANCOISE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: CLAVEL, FRANCOISE
APPLICANT: GORMAN, ANDREM
APPLICANT: GUILLENY, CAROLINE
APPLICANT: GUILLENY, CAROLINE
APPLICANT: GUETARD, DENISE
APPLICANT: GONTAGNIEN, LUC
APPLICANT: DONJON DE SAINT-MARTIN, JACQELINE
APPLICANT: DONJON DE SAINT-MARTIN, JACQELINE
APPLICANT: COHEN, JAQUES
TITLE OF INVENTION: SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 4; I
100.0%; Pred. No. 1.9e+05;
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APPLICATION NUMBER: PCT/FR 95/01391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/08817441 Patent No. 6399294
RESULT 26
US-09-097-194-13
Sequence 13, Application US/09097194
; Patent No. 6359112
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                 APPLICANT: Kapurniotu, Afroditi
APPLICANT: Bernhagen, Juergen
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-097-194-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dunner,
STREET: 1300 I Str
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC OPERATING SYSTEM:
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nes 3; Conserv
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                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KGA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Gaps
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APPLICANT: Buchard J.
APPLICANT: Mitchell, Robert A.
APPLICANT: Calandra, Thierry F.
APPLICANT: Calandra, Thierry F.
TITLE OF INVENTION: INHIBITION OF MIGRATION INHIBITORY
TITLE OF INVENTION: FACTOR IN THE TREATMENT OF DISEASES INVOLVING
TITLE OF INVENTION: CYTOKINE-MEDIATED TOXICITY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/471,546 FILING DATE: 06-JUN-1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          03260.6005-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7815-030
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08471546 Patent No. 6030615
                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFRERNCE/DOCKET NUMBER: 0326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A. 742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
FILING DATE: 20-OCT-1995
                                                                                                                                                                                                                                                                                                                                                         ; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-817-441-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KGA 3
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US-08-925-002-31
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APPLICANT: Granoff, Dan M.
APPLICANT: Granoff, Dan M.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 1238.002
CURRENT APPLICATION NUMBER: US/08/925,002
CURRENT APPLICATION NUMBER: US/08-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 8
                                                                                                                                                                                         USE OF MASS SPECTROMETRY FRACMENTATION
PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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OTHER INFORMATION: Description of Artificial Sequence: sequence from
OTHER INFORMATION: a phage display peptide library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 15; DB 5; Length 7; 100.0%; Pred. No. 1.9e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                    TITLE OF INVENTION: USE OF WASS SPECTROMETRY FRAGMEN
TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABLY
TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABLY
TITLE OF INVENTION: ORGANISMS
NUMBER OF SEQUENCES: 46
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATA:
FILING DATE: 14-MAR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,433
FILING DATE: 14 AMRT.1994
ATTONNEY/AGENT INFORMATION:
NAME: PAIRMELE S. Steven W.
REGISTRATION NUMBER: 31,990
REFENCE/DOKET NUMBER: 16336-2PC
TELEPHONE: 206-467-9600
TELEPAX: 415-543-543
                                                                                                                          Sequence 27, Application PC/TUS9503239 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/08925002
Patent No. 6048527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INPORATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.vv
Thes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide PCT-US95-03239-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                     PCT-US95-03239-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
US-08-925-002-31
                                                                                                                                                                    APPLICANT:
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                                                                            RESULT 22
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GENERAL INFORMATION:
APPLICANT: Repurnictu, Afroditi
APPLICANT: Repurnictu, Afroditi
APPLICANT: Brunner, Juergen
APPLICANT: Brunner, Herwig
TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
TITLE OF INVENTION: In Spongiform Encephalophathies
FILE REFERENCE: US 09/097,194
CURRENT APPLICATION NUMBER: US/09/097,194
CURRENT FILING DATE: 1998-06-12
EARLIER FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 21
SSEQ ID NOS: 21
SSEQ ID NO 12
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                                                                             Gaps
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                           Length 8;
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: ALZHEIMER'S DISEASE
FILE REFERENCE: BU96-09A2
CURRENT APPLICATION NUMBER: US/09/163,095
CURRENT FILING DATE: 1996-09-29
EARLIER APPLICATION NUMBER: PCT/US97/04966
EARLIER APPLICATION NUMBER: 08/625,765
EARLIER PILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%; Score 15; DB 4; Length 8; Similarity 100.0%; Pred. No. 1.9e+05; 3; Conservative 0; Mismatches 0; Indels
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                           100.0%; Score 15; DB 3; I 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 15; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0;
                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 12, Application US/09097194
; Patent No. 6359112
                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09163095; Patent No. 6242416
                                                                           ö
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-163-095-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORGANISM: Homo sapiens US-09-097-194-12
Ouery Match
Best Local Similarity
Local 3; Conserva
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Best Local Similarity
Matches 3; Conserv
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US-09-097-194-12
                                                                                                                        1 KGA 3
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US-09-163-095-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RETHAGEN, Juergen
APPLICANT: Bernhagen, Juergen
APPLICANT: Brunner, Herwig
TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
TITLE OF INVENTION: Peptides Disease, In Type II Diabetes Mellitus And
TITLE OF INVENTION: In Spongiform Encephalophathies
FILE REFRENCE: US 09/097,194
CURRENT PILING DATE: 1998-06-12
CURRENT FILING DATE: 1998-06-12
MUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
         PATTERNS TO IDENTIFY NUCLECTIDE, AMINO ACID OR CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,256
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100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                         CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-MAR-1995
APPLICATION NUMBER: 0S 08/212,433
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: PAIMELE, 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: PAIMELE, 31,990
REGISTRATION NUMBER: 16336-2PC
TELEPHONE: 206-467-9600
TELEPRAX: 415-543-5643
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTER/STICS:
LENGTH: 7 amino acids
TITLE OF INVENTION: PATTERNS TO IDER TITLE OF INVENTION: CARBOHYDRATE SEC TITLE OF INVENTION: ORGANISMS NUMBER OF SEQUENCES: 46 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE OF SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09097194 Patent No. 6359112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-097-194-11
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                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                               Sequence 96, Application US/08397633A
Patent No. 5773577
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
                                                                                                                                    100.0%; Score 15; DB 1; Length 7; 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 15; DB 1; Length 7; 100.0%; Pred. No. 1.9e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                               0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILIG DATE:
CLASSIFICATION: 530
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6017693
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NAME: ROWLAND, 530.
REGISSRATION UNDABER: 20,015
REFERENCE/CDCKET NUMBER: A-58
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 781-1989
TELEFX: (415) 398-3249
TELEX: (910 277299
INFORMATION FOR SEQ ID NO: 96:
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Best Local Similarity 100.
Matches 3; Conservative
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STRANDEDNESS: single
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                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                               single
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94111-4187
         TYPE: amino acid
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APPLICANT:
                           STRANDEDNESS:
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US-08-397-633A-96
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US-08-716-256-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gresham, Hattie D.
APPLICANT: Brown, Eric J.
APPLICANT: Adams, Steven P.
TITLE OF INVENTION: NO. 5225531e1 Hexapeptide
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSE
ADDRESSEE: SCOtt J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh
REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860

INFORMATION FOR SEQ ID NO: 22:
INFORMATION FOR SEQ ID NO: 22:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Patent No. 6359112
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Patent No. 5225531
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-09-392-979A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-097-194-10
                                                                                                                           TYPE: amino acid
                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
US-09-097-194-10
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APPLICANT: Yates, III, John R.
APPLICANT: Brates, III, John R.
APPLICANT: Brates, III, John R.
TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
TITLE OF INVENTION: DATABASES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart St. Tower
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                                                                                                                                                                                                                                    OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,678
FILING DATE: 19920409
CLASSIFICATION NUMBER: 23.0
ATTORNEY/AGENT INFORMATION:
NAME: WAYER, Scott J.
REGISTRATION NUMBER: 25.275
REGISTRATION NUMBER: 07-24(867)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,433A
FILING DATE: 14-MR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: HUGHES, Richard L.
REGISTRATION NUMBER: 31,264
REFERENCE/DOCKET NUMBER: 16336-2
TELECOMMUNICATION INFORMATION:
MINIMAL PROCESSION OF THE PROPERTION OF THE PROPERTIES OF THE PROP
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                                                                          ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELEPRAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-07-866-678-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA ZIP: 94105-1492 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Missouri
                                                     USA
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                                                 COUNTRY:
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LENGIH:

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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-298-017-22
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APPLICANT: SINGH, TEJINDER
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BNHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Law Offices of Peter Dehlinger
STREET: 350
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 15; DB 3; Length 6; 100.0%; Pred. No. 1.9e+05;
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TITLE OF INVENTION: IMPROVED EPIDURAL
TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                             ULEMATING SYSTEM: DOS
SOFTWARE: FASTESED DOS
SOFTWARE: FASTESED for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/613,400A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION INFORMATION:
TELEPRONE: 650-324-0860
TELEFRAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09298017 Patent No. 6087091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              ZIP: 94306-1546
COMPDTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPDTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6 amino a TYPE: amino acid
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                                                                                                   STREET: 350 Camb
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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OPERATING SYSTEMS PACAGES 41.0, Version #1.25

CONGRAPE APPLICATION DATA:

FULLIO DATE:

CHARGET PAPLICATION NAMES:

CHARGET PAPLICATION NAMES:

FULLIO DATE:

FULLIO DATE
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Gaps

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Patent No. 5891849
CENERAL INFORMATION:
APPLICANT: Amsturz, Gary A.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                               CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
                                                                                                                                                                                                         Query Match 100.0%; Score 15; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 15; DB 2; Length 6; 100.0%; Pred. No. 1.9e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
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ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DAN COMPALLADE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-00/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFRAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
  6 amino acids
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                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                             INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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Matches 3; Conserv
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                                                                                                                                                                                                                                                                                               1 KGA 3
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LENGTH:
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                                                                                                         APPLICANT: SUSILE, ALAN
APPLICANT: SUGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTHO, KAREN L
APPLICANT: WILLANICH, GEORGE P
TITLE OF INVENTION: BIHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: BIHANCING OPIATE ANALGESIA AND
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 15; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELEPONGE: (415) 324-0880
TELEPAN: (415) 324-0880
TELEPAN: (415) 324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/08613400A
Patent No. 6054429
GENERAL INFORMATION:
APPLICANT: Bowersox, S. Scott
APPLICANT: Gadbois, Theresa
APPLICANT: Pettus, Mark, R.
APPLICANT: Luther, Robert, R.
                         Sequence 22, Application US/09138439
; Patent No. 2994305
; GENERAL INFORMATION:
    APPLICANT: JUSTICE, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           94306
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US-09-138-439-22
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TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 22:
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0
Best Local Similarity 100.0
Matches 3; Conservative
                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                       ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-742-774-22
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Patent No. 5824645

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JUNCH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILJANICH, GERGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMOFÉLICES OF PEET Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 100.0%; Score 15; DB 1; Length 6; Similarity 100.0%; Pred. No. 1.9e+05; 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
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APPLICATION NUMBER: US/08/742,774
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-UNN 1995
CLASSIFICATION: 514
                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                               94306-1546
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STATE: CA
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                 COUNTRY:
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APPLICANT: JUGTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOLLL, KISHOR C
APPLICANT: GOLLL, KISHOR C
APPLICANT: MILDANICH, GENGE P
APPLICANT: MILDANICH, GENGE P
APPLICANT: MILDANION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: BUHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                      CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 15; DB 2; Length 6; 100.0%; Pred. No. 1.9e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                              APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION 530
PRICAPLICATION DATA: 340
PRICATION NUMBER: US/08/049,794
FILING DATE: 1933-APP.15
APPLICATION NUMBER: US/08/14,759
FILING DATE: 30-DEC-1991
ATONREY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REBERNECE/DOCKET NUMBER: 5865-0009,30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTONEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
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                                                                                                                                         Sequence 22, Application US/07789913
Fatent No. 5559055
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Pox, James A.
APPLICANT: Patner, Robert S.
APPLICANT: Yalentino, Raren L.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
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SOUTHWER: Patentin Release #1.0, Version #1.25
SOUTHWER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-04G-1990
PRIOR APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-000-1989
APPLICATION NUMBER: S895
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: $865-0005,30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 22:
SEQUIENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Law Offices of Peter Dehlinger SYREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 6 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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                                                                                                   RESULT 6
US-07-789-913-22
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US-08-049-794-22
                                          1 KGA 3
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; Sequence 22, Application US/08049794 ; Patent No. 5587454

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Sequence 22, Application US/08496847

Sequence 22, Application US/08496847

Sequence 22, Application US/08496847

GENERAL INFORMATION:

APPLICANT: Amstutz, Gary A.

APPLICANT: Bowersox, Stephen S.

APPLICANT: Gohli, Kishorchandra

APPLICANT: Adriaenseens, Peter I.

APPLICANT: Aristipati, Ramasharma

TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Deblinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TELINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: MILANICH, GEORGE P
APPLICANT: MILANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: LAW Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE INDIVIDUAL ISOLATE: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 15; DB 1; Length 6; ilarity 100.0%; Pred. No. 1.9e+05; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: STOPNY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 amino acids
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYDOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; INDIVIDUAL ISOLATE:
US-08-049-794-22
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                  STATE:
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APPLICANT: Kapurniotu, Afroditi
APPLICANT: Bernhagen, Juergen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 15; DB 4; Length 5; 100.0%; Pred. No. 1.9e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 15; DB 2; Length 5; 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,037A FILING DATE: 24 MAY 1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/09097194; Patent No. 6359112; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Cyclic peptide US-09-163-095-3
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGIERRATION UNDRER: 35.024
REFERENCE/DOCKET NUMBER: 0007
TELECOMMUNICATION INFORMATION:
TELEFAX: 301-504-5676
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
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US-09-097-194-9
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APPLICANT: Brunner, Herwig
TITLE OF INVENTION: Peptides Used As Agonists And/or Inhibitors Of Amyloid
TITLE OF INVENTION: Peptides Used As Agonists And/or Inhibitors Of Amyloid
TITLE OF INVENTION: Portation And Cytotoxicity And Also For Use In
TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
TITLE OF INVENTION: In Spongiform Encephalophathies
FILE REFERENCE: US 09/09/194
CURRENT APPLICATION NUMBER: US/09/097,194
CURRENT FILING DATE: 1998-06-12
EARLIER FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PARCHILL OF THE OFFICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 15; DB 4; Length 5; 100.0%; Pred. No. 1.9e+05;
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APPLICATION NUMBER: US/07/866,678 FILING DATE: 19920409 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh
CITY: St. Louis
COUNTRY: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gresham, Hattie D.
APPLICANT: Brown, Eric J.
APPLICANT: Adams, Steven P.
TITLE OF INVENTION: No. 5225531e1 Hexapeptide
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A35
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ATTORNEY/AGENT INFORMATION:
NAME: Meyer, SCOCT J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24(867)A
TELECOMMUNICATION INFORMATION:
TELECHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07866678 Patent No. 5225531
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Best Local Similarity 100.0
Matches 3; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CRGANISM: Homo sapiens
US-09-097-194-9
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Sequence 6, Appli
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                                                                   9, 2002, 14:11:40 ; Search time 14 Seconds (without alignments) 6.305 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/FB_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-653-037A-6
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US-07-866-678-1
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US-08-049-794-22
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US-09-675-314-22
US-09-675-314-22
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US-09-677-354-22
US-09-097-194-10
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US-09-097-194-11
                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Match Length
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Maximum DB seq length: 20
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| US-08-471-546-1
US-08-159-339A-792
US-08-159-339A-805
US-08-159-339A-817
US-08-471-586-6
US-09-202-832-8
US-09-257-179-112
US-08-757-179-112
US-08-757-179-112
US-08-757-179-112
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US-08-733-148-3
US-08-159-339A-794
US-08-159-339A-835
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US-08-159-339A-846
US-08-925-002-40
US-08-925-002-40
US-09-925-002-40
US-09-9163-095-4 | RESULT 1 US-09-458-481B-15 US-09-458-481B-15 Sequence 15, Application US/09458481B Sequence 15, Application US/09458481B Sequence 15, Application US/09458481B Sequence 15, Application US/09458481B GENERAL INFORMATION: APPLICANT: KUMAR, Vijaya B. TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA FILE REFERENCE: 16153-9250 CURRENT APPLICATION NUMBER: US/09/458,481B CURRENT APPLICATION NUMBER: US/09/458,481B NUMBER OF SED ID NOS: 20 SOFTWARE: PATE: 1999-12-09 SED ID NO 15 LENGTH: 4 TYPE: PRT CORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: GF SEQ ID NO: 9 US-09-458-481B-15 | Score 15; DB 4; Pred. No. 1.9e+05 ; Mismatches (37A) coteinase Deleted Viruses and Their ter (005, BARC-W) |
| 00000000000000000000000000000000000000 | tion US/09458 ligaya B. ATTISENSE MCATISENSE MCABER: US/0 1999-12-09 1999-12-09 1999-12-09 ver. 2.0 al Sequence Description Encoded by c | 100.0%; 100.0%; ative C Marvin J Peter W Marvin Eser W Leader P Le |
| 0.0000000000000000000000000000000000000 | -481B-15 e 15, Applicati No. 631004B INFORMATION: ANT: KUMAR, V1; OF INVENTION: T FILING DATE: T FILING DATE: TOF SEQ ID DATE: RE: PATENTIN VE. NO. 15 PRT ISSM: ATTIFICIAL RE: INFORMATION: DE INFORMATION: DE INFORMATION: DE INFORMATION: OF INFORMATION: O | A 3 Similarity 1 3; Conservati; 1 A 4 A-6 Application U; 5824116 FURNALION: Pett IT: Mason, Pett IT: Mason, Pett IT: Piccone, Marr: Piccone, Marr: Rieder, Ell. INVENTION: Lo. INVENTION: |
| 229
330
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1 | DESULT 1 Second 15, Application U Patent No. 6310048 GENERAL INFORMATION: APPLICANT: KUMAR, Vijaya TITLE OF INVENTION: ANTIS FILE REFERENCE: 16153-925 CURRENT APPLICATION NUMBE CURRENT APPLICATION NUMBE CURRENT APPLICATION NUMBE CURRENT FILING DATE: 199 NUMBER OF SEO ID NOS: 20 SOFTWARE: PATENTIN VET: 2 LENGTH: 4 TYPE: PRT ORGANISM: Artificial Sequentin Nos: 2 CORGANISM: ARTIFICIAL SEGUENTE: OTHER INFORMATION: DESCR. OTHER INFORMATION: DESCR. OTHER INFORMATION: OF SEGUENTE: OTHER INFORMATION: OTHER INFORMAT | Local S. hes 3 1 KGA . 1 KGA . 2 KGA . 2 KGA . 1 H No. 5 1 H |
| | RESULT US-09-4 Seque Representation | Quer. Best Matcl Oy Db Db Seque Pater |



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APPLICANT: Malabathorth, Vladdmir APPLICANT: Malabathorth, Vladdmir APPLICANT: Carr. Peters S.
APPLICANT: Rain, Peters S.
TITLE OF INTERTON: Inthibitors of HIV Membrane Fusion Filter Marker ON.
FILTE OF INTERTON: Inthibitors of HIV Membrane Fusion Filter Marker ON.
FILTE OF INTERCANTON: Malabath (1997) 130 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131 (1997) 131
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Patent No. US20020128175A1
SEMERAL INPORMATION:
APPLICANT: Gattadahalli M. Anantharamaiah
TITLE OF INVENTION: Synthetic Peptides that Enhance LDL Uptake
FILE REFERENCE: D6084
CURRENT PELLING NUMBER: US/09/520,698
CURRENT FILING DATE: 1999-03-17
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 4
LENGTH: 18
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                                                                                              100.0%; Score 15; DB 10; Length 18; 100.0%; Pred. No. 1.40+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: lipid-associating peptide US-09-520-698-4
                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: November 9, 2002, 14:16:58 Job time: 11 secs
ORGANISM: Artificial Sequence FEATURE:
                                    ; OTHER INFORMATION: D-peptide US-09-746-742-68
                                                                                                                                       Conservative
                                                                                              Query Match
Best Local Similarity
Matches 3; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Unknown
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US-09-520-698-4
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NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 18
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                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                      ; OTHER INFORMATION: D-peptide US-09-746-742-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: D-peptide US-09-746-742-65
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US-09-746-742-65
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             APPLICANT: ECKALL, DEDGIAIN M.
APPLICANT: ECKAL, DEDGIAIN M.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Carr, Peter A.
APPLICANT: Carr, Peter A.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399,1192-008
CURRENT FILING DATE: 2000-12-21
FRIOR PAPLICATION NUMBER: DET/US99/17351
FRIOR PILING DATE: 1999-07-30
FRIOR APPLICATION NUMBER: US 60/043,280
FRIOR PILING DATE: 1999-07-30
FRIOR PELING DATE: 1997-04-17
FRIOR PILING DATE: 1998-04-17
FRIOR PILING DATE: 1998-07-30
FRIOR APPLICATION NUMBER: US 60/100,265
FRIOR PELING DATE: 1998-09-14
FRIOR PELING DATE: 1998-09-14
FRIOR FILING DATE: 1998-09-14
FRIOR FILING DATE: 1998-09-14
FRIOR FILING DATE: 1998-09-14
FRIOR FILING DATE: 1998-09-18
FRIOR PELING DATE: 1998-09-18
FRIOR FILING DATE: 1998-09-18
FRIOR FILING DATE: 1998-09-18
FRIOR FILING DATE: 1998-09-18
FRIOR PELING DATE: 1998-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTED fOR Windows Version 4.0
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Patent No. US20020077284A1

GENERAL INFORMATION:

APPLICANT: Eckert, David C.

APPLICANT: Eckert, David C.

APPLICANT: Chan, David C.

APPLICANT: Carr, Peter A.

APPLICANT: Carr, Peter S.

TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion FILE REFERENCE: 1039-1192-008

CURRENT APPLICATION NUMBER: US/09/746,742

CURRENT FILING DATE: 2000-12-21

PRIOR PELIOR DATE: 1999-07-30

PRIOR PELIOR DATE: 1999-07-30

PRIOR APPLICATION NUMBER: US 60/043,280

PRIOR APPLICATION NUMBER: US 60/094,676

PRIOR APPLICATION NUMBER: US 60/100,265

PRIOR FILING DATE: 1998-09-14

PRIOR FILING DATE: 1998-09-14

PRIOR FILING DATE: 1998-09-18

PRIOR PRILING DATE: 1998-09-18

PRIOR PRILING DATE: 1998-09-18

PRIOR PRILING DATE: 1998-09-18

PRIOR PILING DATE: 1998-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(18); OTHER INFORMATION: Xaa = Any Amino Acid US-09-746-742-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: D-peptide NAME/KEY: VARIANT
APPLICANT: Eckert, Deborah M.
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US-09-746-742-64
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| Sequence 65. Application US/09746742
| Patent No. US20020077284A1
| GENERAL INFORMATION:
| APPLICANT: Chan, David C.
| APPLICANT: Chan, David C.
| APPLICANT: Malashkevich, Vladimir
| APPLICANT: Malashkevich, Vladimir
| APPLICANT: Kim, Peter A.
| APPLICANT: Carr, Peter A.
| APPLICANT: Kim, Peter S.
| TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion FILE REFERENCE: 0399.1192-008
| CURRENT FALING DATE: 1990-172-21
| PRIOR PAPLICATION NUMBER: US/09/746,742
| CURRENT FILING DATE: 1997-04-17
| PRIOR FILING DATE: 1998-04-17
| PRIOR FILING DATE: 1998-07-30
| PRIOR PILICATION NUMBER: US 60/100,265
| PRIOR PILING DATE: 1998-07-18
| PRIOR FILING DATE: 1998-09-14
| PRIOR FILING DATE: 1998-09-14
| PRIOR FILING DATE: 1998-09-14
| PRIOR FILING DATE: 1998-09-18
| PRIOR FILING DATE: 1998-09-18
| PRIOR FILING DATE: 1998-09-18
| PRIOR FILING DATE: 1998-05-03
| NUMBER OF SEQ ID NOS: 68
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 65
                                                        Indels
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100.0%; Score 15; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0;
Query Match 100.0%; Score 15; DB 10; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 3; Conservative 0; Mismatches 0;
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                                                                                                                                                                     APPLICANT: ECRETA, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Malashkevich, Vladimir
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FITE REFERENCE: 0399-1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-04-17
PRIOR PELING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR PILING DATE: 1998-07-30
PRIOR PILING DATE: 1998-07-30
PRIOR PELING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR PELING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-14
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-05-03
PRIOR FILING DATE: 1998-09-05-03
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-05-03
PRIOR FILING DATE: 1908-09-05-03
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APPLICANT: Chan, David C.
APPLICANT: Chan, David C.
APPLICANT: Chan, David C.
APPLICANT: Malashkavich, Vladimir
APPLICANT: Ear, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REPERBENCE: 0399,1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-07-30
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                                                                        Sequence 39, Application US/09746742
Patent No. US20020077284A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40, Application US/09746742 Patent No. US20020077284A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: D-peptide US-09-746-742-39
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Best Local Similarity
Matches 3; Conserva
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RESULT 37
US-09-746-742-39
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US-09-746-742-40
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APPLICANT: Chan, David C.
APPLICANT: Chan, David C.
APPLICANT: ALEX, Peter A.
APPLICANT: ALIA, Peter A.
APPLICANT: Kim, Peter A.
TILE OF INVENTION: Inhibitors of HIV Membrane Fusion FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT APPLICATION NUMBER: US 60/043,280
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR APPLICATION NUMBER: US 60/044,676
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-01-17
PRIOR FILING DATE: 1998-01-18
PRIOR FILING DATE: 1998-01-18
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR APPLICATION NUMBER: US 60/132,295
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.4e+02;
Live 0; Mismatches 0;
                                          NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: FrastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09746742
Patent No. US20020077284A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                ; OTHER INFORMATION: D-peptide US-09-746-742-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: D-peptide US-09-746-742-41
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Best Local Similarity 100.0
Matches 3; Conservative
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US-09-746-742-41
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US-09-746-742-55
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Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Rim, Peter A.
APPLICANT: Lim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
100.0%; Score 15; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR PLICATION NUMBER: US 60/043,280
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR PILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-09-14
PRIOR PLICATION NUMBER: US 60/100,265
PRIOR PRIOR DATE: 1998-09-14
PRIOR PLING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
                       PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR PELING DATE: 1998-09-14
PRIOR PELING DATE: 1998-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 18
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: D-peptide US-09-746-742-19
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FILING DATE: 1998-07-30
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US-09-746-742-38
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LENGTH: 18
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                                                                                                                                                                                                             Sequence 17, Application US/09746742

Patent No. US200200772841

GENERAL INFORMATION:

APPLICANT: Eckert, Deborah M.

APPLICANT: Eckert, Deborah M.

APPLICANT: Carr, Peter A.

APPLICANT: Malashkevich, Vladimir

APPLICANT: Kim, Peter S.

TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008

CURRENT FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-04-17

PRIOR FILING DATE: 1999-04-17

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1998-09-18

PRIOR FILING DATE: 1998-09-18
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Patent No. US20020077284A1

GENERAL INFORMATION

APPLICANT: Chan, David C.

APPLICANT: Chan, David C.

APPLICANT: Malashkevich, Vladimir

APPLICANT: Malashkevich, Vladimir

APPLICANT: Kim, Peter S.

TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

FILE REFERENCE: 0399-1192-008

CURRENT APPLICATION NUMBER: US/09/746,742

FRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: US 60/043,280

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1998-04-17

PRIOR PLILING DATE: 1998-04-17

PRIOR PLILING DATE: 1908-04-17
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Matches 3; Conservative
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US-09-746-742-19
                                                                         16 KGA 18
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             1 KGA 3
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RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Chan, David C.
APPLICANT: Chan, David C.
APPLICANT: Carr, Peter A.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR APPLICATION NUMBER: US 60/044,676
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR PILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 15; DB 10; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 3; Conservative 0; Mismatches 0;
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                                                                               NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 16
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09746742
Patent No. US20020077284A1
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US-09-746-742-18
; Sequence 18, Application US/09746742
; Patent No. US20020077284A1
                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: D-peptide US-09-746-742-15
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US-09-746-742-16
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2 KGA 4
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SGENERAL INFORMATION:

APPLICANT: ECKET, Deborah M.

APPLICANT: ECKET, Deborah M.

APPLICANT: Malashkevich, Vladimir

APPLICANT: Malashkevich, Vladimir

APPLICANT: Kim, Peter A.

APPLICANT: Kim, Peter S.

TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

FILE REFERENCE: 0399:1192-008

CURRENT APPLICATION NUMBER: US/09/746,742

CURRENT APPLICATION NUMBER: US/09/746,742

PRIOR APPLICATION NUMBER: US 60/043,280

PRIOR APPLICATION NUMBER: US 60/043,280

PRIOR PILING DATE: 1999-04-17

PRIOR APPLICATION NUMBER: US 60/04,676

PRIOR APPLICATION NUMBER: US 60/100,265

PRIOR APPLICATION NUMBER: US 60/101,058

PRIOR APPLICATION NUMBER: US 60/101,058

PRIOR APPLICATION NUMBER: US 60/13,295

PRIOR APPLICATION NUMBER: US 60/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: D-peptide
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Matches 3; Conserva
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TYPE: PRT ORGANISM: Artificial Sequence
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|13 KGA 15
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Sequence 9, Application US/09996357

Sequence 9, Application US/09996357

Sequence 9, Application US/09996357

GENERAL INFORMATION:

APPLICANT: Gefter, Malcolm L

APPLICANT: Isreal, David I

APPLICANT: Gosselin, Michael

TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE

FILE REFERENCE: PPI-105

CURRENT EILING DATE: 2000-11-27

CURRENT EILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PLICATION NUMBER: 60/253,302

PRIOR FILING DATE: 2000-11-27

PRIOR PRIOR FILING DATE: 2000-11-27

PRIOR PRIOR FILING DATE: 2000-11-27

PRIOR PRIOR FILING DATE: 2000-11-29
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                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/972,475

FILMG DATA:

APPLICATION NUMBER: 08/617,267

FILMG DATE: O7-JUN-1995

APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DECORT, GIULIO A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECTUE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 15 amino acids TYPE: amino acid
                                                     STATE: Massachusetts
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 15
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                              CITY: Boston
                                                                            COUNTRY: USA
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Page 7

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US-09-873-459A-26
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US-09-972-475-14
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Patent No. US20020064533A1
GENERAL INFORMATION:
APLICANT: Murray, Kenneth
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
PRIOR PAPLICATION NUMBER: PCT/US99/28755
PRIOR PAPLICATION NUMBER: 60/110,911
PRIOR APPLICATION NUMBER: 60/110,911
             APPLICANT: MILTRAY, Kenneth
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-04
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Patent No. US20020064533A1
GENERAL INFORMATION:
APPLICANT: Murray, Kenneth
TILE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: HBV OTHER INFORMATION: capsid-binding peptide US-09-873-459A-24
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100.0%; Pred. No. 1.2e+02;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 15
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 15
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Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
GENERAL INFORMATION:
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US-09-873-459A-26
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Sequence 27, Application US/09873459A

Sequence 27, Application US/09873459A

Sequence No. US20020064533A1

GENERAL INPORMATION:

TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS

FILE REFERENCE: A067 CIP

CURRENT APPLICATION NUMBER: US/09/873,459A

CURRENT APPLICATION NUMBER: PCT/US99/28755

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-04

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 27

LENGTH: 15
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         COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09972475
Patent No. US20020098173A1
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: HBV OTHER INFORMATION: capsid-binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: HBV CHER INFORMATION: capsid-binding peptide US-09-873-459A-27
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA F FILE REPERENCE: A067 CIP CURRENT APPLICATION NUMBER: US/09/873,459A; CURRENT FILING DATE: 2001-09-17 PRIOR APPLICATION NUMBER: PCT/US99/28755 PRIOR FILING DATE: 1999:12-03 PRIOR FILING DATE: 1998:12-04 NUMBER OF SEQ ID NOS: 47 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 SECTION NO.
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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GENERAL INFORMATION:
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                                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

TITLE OF INVENTION: GOMPONENTS ATTACHED VIA PEPTIDE LIGANDS

TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS

FILE REFERENCE: A067 CIP

CURRENT APPLICATION NUMBER: US/09/873,459A

CURRENT FILING DATE: 2001-09-17

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 47

SOFTWARRE: PATCHIN VET. 2.1

SED ID NO 20
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%Sequence 21, Application US/09873459A
%Sequence 21, Application US/09873459A
%Sequence 21, Application US/09873459A
%Sequence 21, Application CONCOMPATION:
%APPLICANT: MULTAP, Kenneth
%TITLE OF INVENTION: HOW CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
%TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
%TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
%TITLE OF INVENTION OF CONCOMPAGE: 2001-09-17
%CURRENT PALLING DATE: 2001-09-17
%PRIOR FILING DATE: 1999-12-03
%PRIOR FILING DATE: 1999-12-04
%PRIOR FILING DATE: 1999-12-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:HBV
OTHER INFORMATION: capsid-binding peptide
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                    Sequence 20, Application US/09873459A
Patent No. US20020064533A1
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 15
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Matches 3; Conserva
US-09-873-459A-20
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RESULT 21

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US-09-873-459A-22

| Sequence 22, Application US/09873459A |
| Patent No. US200064533A1 |
| GENERAL INFORMATION: |
| APPLICANT: MULTAY, Kenneth |
| TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS |
| FILE REFERENCE: A067 CIP |
| CURRENT APPLICATION NUMBER: US/09/873,459A |
| CURRENT PAPLICATION NUMBER: PCT/US99/28755 |
| PRIOR APPLICATION NUMBER: 60/110,911 |
| PRIOR FILING DATE: 1998-12-04 |
| NUMBER OF SEQ ID NOS: 47 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 22 |
| LENGTH: 15
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TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT FILING DATE: 2010-109-17
PRIOR FILING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 47
SSOFTWARE: PATENTIN VET: 2.1
SSOFTWARE: PATENTIN VET: 2.1
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0;
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Fatent No. US2020064533A1
GENERAL INFORMATION:
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REPERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT PAPLICATION NUMBER: PCT/US99/28755
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR APPLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SOCYMARE: Patentin Ver: 2.1
SEQ ID NO 38
LENGTH: 14
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APPLICANT: RASTELL, LUCA
APPLICANT: PENNECA, DIANE
TITLE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 10716.36
CURRENT APPLICATION NUMBER: US/09/815,248
CURRENT FILING DATE: 2001.08-20
PRIOR PELING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PELING Ver. 2.1
SEQ ID NO 16
LENGTH: 14
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                                                                                                                  CTHER INFORMATION: Description of Artificial Sequence: HBV CTHER INFORMATION: capsid-binding peptide US-09-873-459A-40
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                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity luv...
3; Conservative
SOFTWARE: PatentIn Ver. 2.1
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US-09-873-459A-38
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US-09-815-248-16
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                SEQ ID NO 40
LENGTH: 12
                                                          PRT
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Sequence 5. Application US/09865644

Patent No. US20020045188A1

GENERAL INFORMATION:

APPLICATT Kamb et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION UNMBER: US/09/865,644

CURRENT FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 5

LENTH: 15

LENTH: 15
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APPLICANT: RASTELLI, LUCA
APPLICANT: PENNICA:
TITLE OF INVERTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 10716.36
CURRENT APPLICATION NUMBER: US/09/815,248
CURRENT PELING DATE: 2001-08-20
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 38
SOFTWARRE: PATENTIN Ver. 2.1
SEQ ID NO 20
LENGTH: 14
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OTHER INFORMATION: Description of Artificial Sequence: Illustrative; OTHER INFORMATION: peptide US-09-815-248-16
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100.0%; Score 15; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09815248 Patent No. US20020098540A1
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US-09-865-644-5
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-815-248-20
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US-09-865-644-5
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Sequence 19, Application US/09873459A
Sequence 19, Application US/09873459A
Sequence 19, Application US/09873459A
Sequence 19, Application US/09873459A
GENERAL INFORMATION:
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT PILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
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TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PC/1059/28755
PRIOR APPLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENDIN: 12
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; OTHER INFORMATION: Description of Artificial Sequence: HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-18
                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence: HBV COTHER INFORMATION: capsid-binding peptide US-09-873-459A-13
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
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ORGANISM: Artificial Sequence
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Matches 3; Conserva
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TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT FILNG DATE: 2001-09-17
PRIOR PILING DATE: 1099-12.03
PRIOR FILING DATE: 1999-12.04
NUMBER OF FULLING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
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APPLICANT: MITTAY, Kenneth
TITLE OF INVENTION: HOW CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A667 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 47
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                                                                                                                                                                                                                                                                                                    DB 10; Length 12; 95;
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; Patent No. US20020064533A1
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 19
LENGTH: 12
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ORGANISM: Artificial Sequence
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US-09-873-459A-40
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LENGTH: 12
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Sequence 36, Application US/09873459A

Sequence 36, Application US/09873459A

Sequence 36, Application US/09873459A

Sequence 36, Application US/09873459A

GENERAL INFORMATION:

APPLICANT: Murray, Kenneth

TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS

FILE REFERENCE: A067 CIP

CURRENT APPLICATION NUMBER: DCJ-09-17

PRIOR APPLICATION NUMBER: PCJ-039/28755

PRIOR APPLICATION NUMBER: E07/10911

PRIOR APPLICATION NUMBER: 60/110,911

PRIOR PLING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 36

LENGTH: 10
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TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REPERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
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FILE REFERENCE: A067 CIP
CURRENT PAPLICATION NUMBER: US/09/873,459A
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR APLICATION NUMBER: PCT/US99/28755
PRIOR APLICATION NUMBER: 60/110,911
PRIOR APLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 9
LEMETH: 10
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ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: Murray, Kenneth
TITLE OF INVENTION: HBY CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOCENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
CURRENT FILING DATE: 1299-12-03
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR APPLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-04
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Partent No. US20020064333A1
GENERAL INFORMATION:
APPLICANT: Murray, Kenneth
TILLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:HBV
OTHER INFORMATION: capsid-binding peptide
NAME/KEV: MOD_RES
LOCATION: (11)
OTHER INFORMATION: bala
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 10
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                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 12
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US-09-873-459A-13
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Sequence 9, Application US/09873459A
Patent No. US20020064533A1
GENERAL INFORMATION:
APPLICANT: Murray, Kenneth
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS FILE REFERENCE: A067 CIP CURRENT APPLICATION NUMBER: US/09/873,459A CURRENT FILING DATE: 2001-09-17 PRIOR APPLICATION NUMBER: PCT/US99/28755 PRIOR APPLICATION NUMBER: PCT/US99/28755 PRIOR APPLICATION NUMBER: 60/110,911 PRIOR RILING DATE: 1998-12-04 NUMBER OF SEQ ID NOS: 47 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6 LENGTH: 9
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Best Local Similarity 100.0%; Score 15; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 3; Conservative 0; Mismatches 0; Indels
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Patent No. US20020051988A1
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APPLICANT: Gilchrest, Barbara A.
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US-09-873-459A-9
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                                                            APPLICANT: GALCHAESL, CALLAGE APPLICANT: Yaar, Mina APPLICANT: Yaar, Mina TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING TITLE OF INVENTION: ALZHEIMER'S DISEASE FILE REPERENCE: BUJ6-09A2 CURRENT APPLICATION NUMBER: US/09/866,898 CURRENT APPLICATION NUMBER: 09/163,095 PRIOR APPLICATION NUMBER: 09/163,095 PRIOR APPLICATION NUMBER: 09/163,095 PRIOR APPLICATION NUMBER: 09/29 PRIOR APPLICATION NUMBER: 08/625,765 PRIOR APPLICATION NUMBER: 08/625,76
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                                                 APPLICANT: Gilchrest, Barbara A.
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Matches 3; Conservative
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; ORGANISM: Homo sapiens
US-09-866-898-1
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US-09-729-835-112
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US-09-729-835-112
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 112, App Sequence 6, Appli Sequence 4, Appli Sequence 9, Appli Sequence 36, Appli Sequence 10, Appl Sequence 3, Appli Sequence 1, Appli Sequence 1 Sequence 1 Sequence 1 Sequence Sequence Description Sequence Sequence Sequence Sequence US-09-866-898-3 US-09-86-898-11 US-09-720-83-112 US-09-873-459A-6 US-09-873-459A-36 US-09-873-459A-36 US-09-873-459A-10 US-09-873-459A-11 US-09-873-459A-11 US-09-873-459A-11 US-09-873-459A-11 US-09-873-459A-19 US-09-873-459A-19 US-09-873-459A-19 US-09-873-459A-10 SUMMARIES H Query Match Length DB 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.001 Score Result ٠ و

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                                                                                     APPLICANT: GILCHEST, BAIDATA A.
APPLICANT: GILCHEST, BAIDATA A.
APPLICANT: GILCHEST, MINA
TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: ALZHEIMER'S DISEASE
FILE REFERENCE: BU96-09A2
CURRENT APPLICATION NUMBER: 09/163,095
PRIOR APPLICATION NUMBER: 09/163,095
PRIOR APPLICATION NUMBER: PCT/US97/04966
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-03-28
PRIOR FILING DATE: 1998-03-28
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ. ID NOS: 5
SUFTANE: FASTSEQ for Windows Version 3.0
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Similarity 100.0%; Pred. No. 7.7e+04;
3; Conservative 0; Mismatches 0;
                      Sequence 3, Application US/09866898; Patent No. US20020051988A1; GENERAL INFORMATION:
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Matches 3; Conserv
US-09-866-898-3
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RESULT 2 US-09-866-898-1

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Sequence 1, Application US/09866898 Patent No. US20020051988A1 GENERAL INFORMATION:

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ORGANISM: Artificial sequence

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Sequence 99, Application US/10211088
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Bright, Gary R.
APPLICANT: Prenkumar, D. David
APPLICANT: Chen, Vih-Tai
APPLICANT: Chen, Vih-Tai
APPLICANT: Chen, Vih-Tai
APPLICANTION: Novel Fusion Proteins And Assays For Molecular Binding
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2001-0-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR APPLICATION NUMBER: 60/301,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF ESC ID NOS: 366
SOFTWARE: PatentIn version 3.1
LENGTH: 14
TYPE: PRT
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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COTHER INFORMATION: Binding domain
US-10-211-088-99

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Best Local Similarity 100.0%; Score 15; DB 6; Length 14;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: November 9, 2002, 14:16:41
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  Q9TRF5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Lipid transfer protein (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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Liu F., Charlesworth D., Kreitman M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
EMBL; AF054493; AAC19033.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Leavenworthia.
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SEQUENCE.
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Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Class I cytochrome C isoform B (Fragment).
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SEQUENCE 15 AA; 1581 MW; 6F7F95A003BA22E3 CRC64;
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Zhang J.R., Hardham J.M., Barbour A.G., Norris
"Antigenic variation in Lyme disease borreliae
recombination of VMP-like sequence cassettes.";
Cell 89:275-285(1997).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative vls recombination cassette Vls14a (Fragment).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                       Candida parapsilosis (Yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharon
Saccharomycetales; mitosporic Saccharomycetales; Candida
NCBI_TaxID-5480;
                                                                     the yeast Candida parapsilosis.";
Biochim. Biophys. Acta 1143:135-141(1993).
SEQUENCE 19 AA; 2108 MW; 17023D754FF25F87 CRC64;
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                                                                                                                                                                           Camougrand N., Velours J., Denis M., Guerin M., "Isolation, characterization and function of th
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SEQUENCE 20 AA; 1923 MW; D0574C31688AB4D7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
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Mammalia; Eutheria;
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OM protein - protein search, using sw model

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Perfect score: GUCKER-1 15 1 kga 3

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SUMMARIES

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ALIGNMENTS

R:Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Etherton, T.D.
Comp. Biochem. Physiol. B 92, 561-567, 1989
A;Title: Purlfication of the serum acid-stable insulin-like growth factor binding protein A;Reference number: A60528; MUID:89209787; PMID:2468442
A;Recession: A60528
A;Status: preliminary insulin-like growth factor-binding protein, serum - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60528 A; Molecule type: protein A; Residues: 1-12 <WAL> RESULT 1

unidentified QM0023 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998 calotropin DI - mudar (fragment)
C;Species: Calotropis gigantea (mudar, madar)
C;Bate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: PT0026
R;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
Phytochemistry 26, 633-636, 1987
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calo A;Reference number: PT0026 밁 Qy A; Experimental source: neuroblastoma cell C; Comment: The molecular mass is 30,500 and the pI is 6.19. A; Reference number: PN0041 A; Accession: PN0048 A; Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne R; Kato, H C; Accession: PN0048 PN0048 Вb δÃ C; Keywords: brain A; Molecule type: protein A; Residues: 1-13 <KAT> Kawasaki Igakkaishi 22, 245-259, 1996 cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Species: Pusarium sporotrichioides
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0087
R;Chow, L. P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotr RESULT 4 PA0087 A;Residues: 1-14 <BHA> C;Comment: This enzyme is classified as a plant cysteine protease. C;Keywords: pyroglutamic acid C;Keywords: pyroglutamic acid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental A; Molecule type: protein A; Residues: 1-14 <BHA> RESULT 3 B QУ A; Accession: PT0026 A; Accession: PA0087 A; Reference number: PA0051 Matches Best Local Similarity Query Match Matches Best Local Similarity Query Match Matches Query Match 1 KGA 3 2 KGA 4 11 KGA 13 4 KGA 6 1 KGA 3 Local Similarity 1 KGA 3 ω,.. Conservative 100.0%; Score 15; DB 2; illarity 100.0%; Pred. No. 3.8e+0; Conservative 0; Mismatches Conservative 100.0%; Score 15; DB 2; 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0; 100.0%; Score 15; DB 2; 100.0%; Pred. No. 3.5e+02; 0; Mismatches . 3.8e+02; ches 0; Length 12; Length 14; Length 13; Indels Indels Indels 0; 0; 0 Gaps Gaps 0: 0

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Ca2+-transporting ATPase (EC 3.6.3.8), cardiac muscle - dog (fragment) c;Species: Canis lupus familiaris (dog) C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 19-Apr-2002 Accession: A24345

PT.198, F.N.; Cable, M.B.; Geisow, M.G.; Green, N.M.
                                                                                                               RESULT 7
A24345
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                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X60839; NID:g53883; PIDN:CAA43232.1; PID:g53884 A;Experimental source: T lymphocyte C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-16 < CAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: T cell receptor genes in a series of class I major histocompatibility complex-allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L. J. Exp. Med. 174, 1371-1383, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell receptor beta chain (RA10.3.3) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experi
A; Note:
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(Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A53085
R:KO, K.W.; Olkawa, K.; Ohnishi, T.; Kay, C.M.; Yokoyama, S.
Biochemistry 32, 6729-6736, 1993
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C;Keywords: electron transfer; heme; photosynthesis
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Pred. No. 4.2e+02;
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A;Gene: CYP4A2
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; t:
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A;Title: Purification and NH2-terminal sequence of cytochrome P-450 from kidney micro
A;Reference number: A26380; MUID:87100198; PMID:3801020
                                                                                                                                                              C; Genetics:
                                                                                                                                                                        A; Contents: annotation; identification of constitutive kidney form as CYP4A2
                                                                                                                                                                                                     A;Reference number: A32966; MUID:89356272; PMID:2766933
                                                                                                                                                                                                          DNA 8, 517-525, 1989
A; Title: The rat clofibrate-inducible CYP4A subfamily II. cDNA sequence of IVA3, mapp
                                                                                                                                                                                                                                                               R;Kimura, S.; Hardwick, J.P.; Kozak, C.A.; Gonzalez, F.J.
                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-20 < IMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: A26380
R; Imaoka, S.; Funae, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Mar-1999
                                                                                                                                                                                                                                                                                               A;Experimental source: kidney, untreated rats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N; Contains: oxidoreductase (EC
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B48408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992
A;Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21K high mobility group protein, hepatic (isoform 2) - Atlantic salmon (fragment) c;Species: Salmo salar (Atlantic salmon) C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997 C;Accession: B48408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-18 <BRI>
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding doma
C;Keywords: ATP; cardiac muscle; heart; hydrolase; muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords:
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A;Title: Primary structure of the nucleotide binding domain of the Ca,Mg-ATPase from A;Reference number: A24345; MUID:86186850; PMID:2938585
A;Accession: A24345
    Matches
                                              Query Match
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              100.0%; Score 15; DB 2; 100.0%; Pred. No. 5.2e+02;
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DE CALOLT
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OC Eukary
OC Sperma
OC Ascler
OC Ascler
CAC 11-FCB
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CAC 11-FCB
CAC 11-FCB
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CC -!-SI
DR PICE;
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                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calotropin DI (EC 3.4.22.-) (Fragment).
Calotropis gigantea (Madar) (Bowstring hemp).
Calotropis gigantea (Madar) (Bowstring hemp).
Calotropis yiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;
                                                                               NCBI_TaxID=4066;
                                                                                                                                                                                                                          Asclepiadeae; Calotropis.
InterPro; IPR000169; SHprot_acsite.
proSITE; pS00139; THIOL_PROTEASE_CYS;
pROSITE; pS00639; THIOL_PROTEASE_HIS;
                                                    PIR; PT0026; PT0026. MEROPS; C01.011; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compus
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                                                                                                                                                      Sengupta A.,
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12.443 Million cell updates/sec
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RESULT 2
ATPB_CANFA
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Best Local
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15-JUL-1998
15-JUL-1998
15-JUN-2002
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MOD_RES 1 1
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Canis familiaris (Dog).
Chordata; Craniata; Vertebrata;
Cranidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                   dog heart proteins.;
Electrophoresis 18:2795-2802(1997).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
-!- FUNCTION: APPORT THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vercebia-a,
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                                                                 HSC-2DPAGE; P99504; DOG.
InterPro; IPR000194; ATPASE_A/bcentre.
PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
                                                                                                                                                                                                                                                 H(+)(Out).

**GUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(COMPONENTS AND COMPONENTS: A, B AND COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                         "HSC-2DPAGE and the two-dimensional gel electrophoresis database
                                                                                                                                                                                                                                                                                                                                                                                                        Dunn M.J., Corbett J.M., Wheeler C.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                     SEQUENCE
                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                  NON_TER
                                                                                                                             UNSURE
                                                                                                                                             UNSURE
                                                                                                                                                                   ATP synthesis; CF(1); Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP +
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 9
                          1 KGA 3
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                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY
 KGA 11
                                                  Similarity
3; Conserv
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(Rel. 41, Last annotation update)
e beta chain, mitochondrial (EC 3.6.3.14) (Fragment).
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1715 MW;
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Pred. No. 1.5e+02;
; Mismatches 0;
                                                                                                        BB9C163FDC60BB42 CRC64;
                                                                   Pred. No.
                                                                              Score 15;
                                                       Mismatches
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                                                                   2e+02;
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                                                                              DB 1; Length 19;
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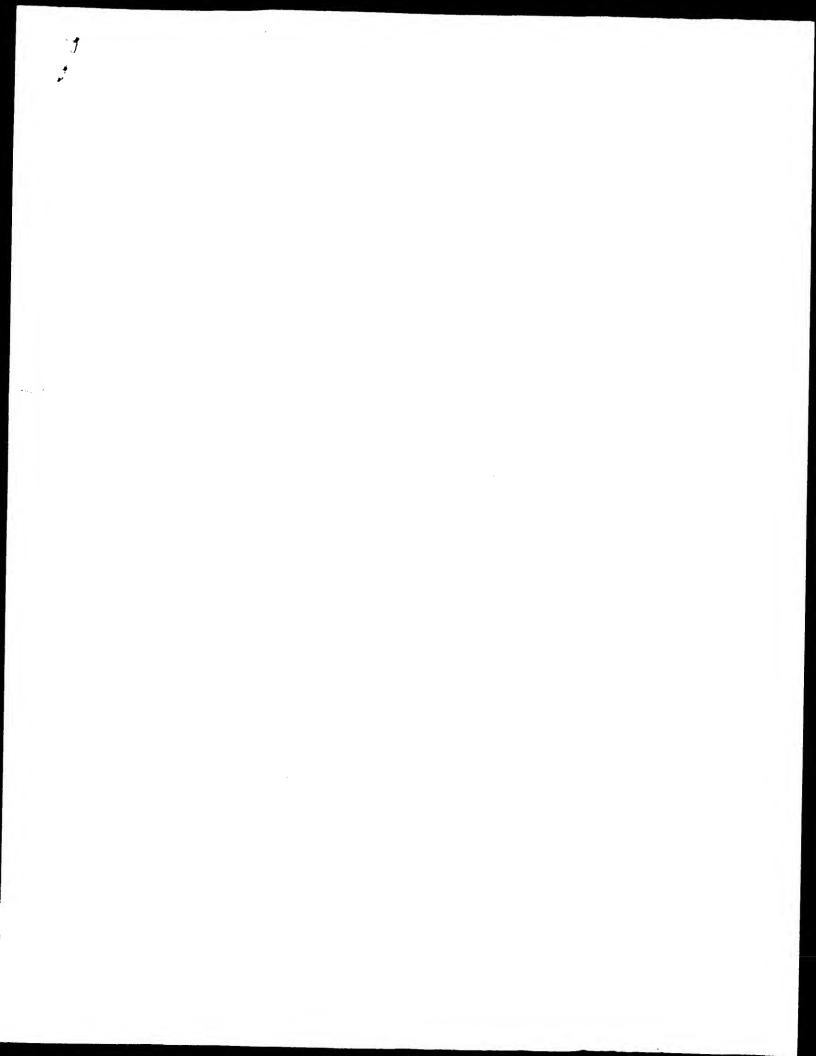
Search completed: November Job time : 10 secs

9

14:12:52

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Qy 1 KGA 3
Db 16 KGA 18

RESULT 10
S68617
histone H2A - sea urchin (Hemicentrotus pulcherrimus) (fragment)
C:Species: Hemicentrotus pulcherrimus) 12-Dec-1997 #text_change 30-Jan-1998
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C:Accession: 568617
R:Ohtsuki, K.; Nishikawa, Y.; Saito, H.; Munakata, H.; Kato, T.
R:Statett 378, 115-120, 1996
A:TEBS Lectt 378, 115-120, 1996
A:Reference number: 588615; MUID:96140721; pMID:8549815
A:Accession: 568617
A;Residues: 1-20 CoHTP
A;
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133 CLGAIC 138

1 CKGAIC 6

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RESULT 15
US-09-372-448A-2
; Sequence 2, Application US/09372448A
; Patent No. 6313376
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
APPLICANT: Francois Chaumont
; APPLICANT: Francois Chaumont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Widolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
VUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 288
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 288
TYPE: PRT
ORGANISM: Zea mays
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US-09-372-422A-12
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Best Local :
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APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 CLGAIC 142
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83.3%;
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83.3%;
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Pred. No. 2.5e+02;
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FITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 1172
CURRENT APPLICATION NUMBER: US/09/372,448A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/096,627
PRIOR FILING DATE: 1998-08-14
NUMBER OF SEO ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 288
TYPE: PRT
ORGANISM: Zea mays
US-09-372-448A-2
Query Match
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps
Matches 5; Conservative 0; Mismatches 1; Indels 04
OR 1 CKGAIC 6
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Db 143 CLGAIC 148
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Search completed: November 9, 2002, 14:04:25 Job time: 9.84615 secs

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TYPE: PRT
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US-09-053-702-2
US-09-053-702-2

Sequence 2, Application US/09053702

Patent No. 6229069

GENERAL INFORMATION:
APPLICANT: YAMADA, Shigehiro

TILLE OF INVENTION: METHOD FOR CONTROLLING WATER CONTENT OF PLANT

FILE REPRESENCE: 230-122P

CURRENT APPLICATION UMBER: US/09/053,702

CURRENT FILING DATE: 1998-04-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 30; DB 1; Length 73; 83.3%; Pred. No. 75; 1; Indels tive 0; Mismatches 1; Indels
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APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/372,422A CURRENT FILING DATE: 1999-08-11 PRIOR APPLICATION NUMBER: US 60/098,692 PRIOR FILING DATE: 1998-08-31 NUMBER OF SEQ ID NOS: 49 SOFTWARE: FASTERQ for Windows Version 3.0
                                                                        NAME: ZIGLINSKI, Bryan
REGISTRATION NUMBER: 34,462
REFERENCE/DOCKET WUMBER: PC8175A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 573-4585
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
                 APPLICATION NUMBER: PCT/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09372422A Patent No. 6313375
                                                                                                                                                                                                                                                                                                                                                                                                         Filistata hibernalis
FILING DATE: 21-MAY-1992
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TISSUE TYPE: venom US-08-379-538-7
                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                       linear
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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ORGANISM: Fil
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68 CLGAIC 73
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                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-09-372-422A-6
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                81.1%; Score 30; DB 4; Length 281; 83.3%; Pred. No. 2.5e+02;
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09372422A

Patent No. 6313375;
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
TILLE OF INVENTION: Maize Aquaporins and Uses Thereof;
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A

CURRENT APPLICATION NUMBER: US 60/098,692

PRIOR FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Chaumont
APPLICANT: Maarten Chrispeels
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 1172
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/372,448A CURRENT FILING DATE: 1999-08-11 PRIOR APPLICATION NUMBER: US 60/096,627 PRIOR FILING DATE: 1998-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 7
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 284
                                                                         ; TYPE: PRT
; ORGANISM: Mesembryanthemum crystallinum
US-09-053-702-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/09372448A; Patent No. 6313376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3.
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                    Best_Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
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                                                                                                                                                                                                                                                 138 CLGAIC 143
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                                                                                                                                                                                                                           1 CKGAIC 6
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US-09-372-422A-8
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US-09-372-448A-4
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                                   SEQ ID NO 2
LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ALVES, KENNETH
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: GUPTA, SUNIL K.
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TILLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CONRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
STATE: NJ
COUWTRY: USA
ZIP: USA
                                         COMPUTER READBREE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 2; 1
Pred. No. 3.8e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application PC/TUS9507295 GENERAL INFORMATION:
                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 536
ATTORNEY FAGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFREENCE/DOCKET NUMBER: 1924
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4462
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 amino acids
TYPE: amino acid
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66.7%; Pred
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NAME: APPOLLINA, MARY A
REGISTATION UNDRER: 34,087
REFERENCE/DOCKET NUMBER: 19244
REFERENCE/DOCKET 19244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.8
Best Local Similarity 66.7
Matches 4; Conservative
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MOLECULE TYPE: protein
US-08-765-243-8
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      USA
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COUNTRY: US.
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PCT-US95-07295-8
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APPLICANT: Pauli, Benedicht U.
TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
FILE REFERENCE: 18617.0052
CURRENT APPLICATION NUMBER: US/09/193,562D
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US/60/065,922
PRIOR FILING DATE: 1997-11-17
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Patent No. 5804554

GENERAL INFORMATION:
APPLICANT: Volkmann, Robert A.
APPLICANT: Saccomano, Nicholas A.
APPLICANT: Racomano, Nicholas A.
APPLICANT: Rosou II, Deane M.
APPLICANT: Robert T.
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
TITLE OF INVENTION: FROM FILISTATA HIBERNALLS
NUMBER OF SEQUENCES;
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.8%; Score 31; DB 4; Length 1000;
83.3%; Pred. No. 5e+02;
iive 0; Mismatches 1; Indels
                                                                             Length 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,538
FILING DATE: 3-MAY-1995
                                                                             Score 31; DB 5; 1
Pred. No. 3.8e+02;
1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 3-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887073
                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/09193562D Patent No. 6309857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pfizer Inc
STREET: 235 East 42nd Street
                                                                                83.8%;
                                                                             Query Match 83.8
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 5; Conservative
                 MOLECULE TYPE: protein
PCT-US95-07295-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-193-562D-30
linear
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: New York
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US-09-193-562D-30
TOPOLOGY:
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LENGTH: 1000
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US-08-379-538-7
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US-08-765-243-2
Sequence 2, Application US/08765243
Sequence 2, Application US/08765243
Sequence 2, Application
Seneral INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: ALVESTON OF THE SEQUENCES:
AUDMESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
COLTY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
                                                                                                        FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REPERENCE/POCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4720
INFORMATION FOR SED ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRENDEDNESS: Single
                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 651 amino acids
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Matches 4; Conservative
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; MOLECULE TYPE: protein
c_US-08-765-243-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CKGAIC 6
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           Length 651;
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
YOMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
           83.8%; Score 31; DB 2; I
66.7%; Pred. No. 3.5e+02;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TILLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19244Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08765243 Patent No. 5935578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: AFPOLLINA, WARPY A
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 1924
TELEPHONICATION INFORMATION:
TELEPHONE: (908)594 3462
TELEPHONE: (908)594 -4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908)594-*/20
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACTERISTICS:
FRNGTH: 651 amin acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 6b./*
Query Match
Best Local Similarity 66./*
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; TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07295-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/25,655
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SED ID NO 5784
LENGTH: 18
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                                                                                                                                                                                                                                                             75.7%; Score 28; DB 9; Length 316; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           0; Indels
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 214
LENGTH: 316
TYPE: PRT
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US-09-815-242-12780
; Sequence 12780, Application US/09815242
; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5784, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5784
                                                                                                                                                                                           ; ORGANISM: Helicobacter pylori
US-09-895-913A-214
                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0
Matches 5; Conservative
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Matches 4; Conservative
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26 KGAIC 30
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US-09-815-242-5784
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GENERAL INVORMATION:
APPLICANT: Haselbeck, Rari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Carr, Crant J.
APPLICANT: Carr, Crant J.
APPLICANT: APPLICANT: Carr, Crant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Daniel: 2001-21
PRICE REPERENCE: ELITRA, 011A
CURRENT FILING DATE: 2000-03-21
PRICE APPLICATION NUMBER: 60/206, 848
PRICE APPLICATION NUMBER: 60/206, 848
PRICE APPLICATION NUMBER: 60/207, 727
PRICE PRICE DATE: 2000-05-26
PRICE FILING DATE: 2000-10-23
PRICE PLICE DATE: 2000-10-23
PRICE PLICE DATE: 2000-11-27
PRICE PLICE DATE: 2000-11-27
PRICE PLICE DATE: 2000-11-27
PRICE PLICE DATE: 2000-11-27
PRICE APPLICATION NUMBER: 60/253,625
PRICE PLICE DATE: 2001-10-23
PRICE APPLICATION NUMBER: 60/253,625
PRICE PLICE DATE: 2001-10-23
PRICE REPERENCE: Estable DATE: 2001-10-23
PRICE APPLICATION NUMBER: 60/253,625
PRICE APPLICATION
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FILING DATE:
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US-08-424-550B-38
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                         APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Al-Garawi, Amal APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles SPELICANT: Miller, Charles SPELICANT: Miller, Charles SPELICANT: Tomb, Jean-Francois APPLICANT: Tomb, Jean-Francois TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Genome FILE REFERENCE: 06132/041002 FILE REFERENCE: 06132/041002 FILE REFERENCE: 06132/041002 FILE REFERENCE: 06132/041002 FILE REFERENCE: 1997-04-01 SPIOR FILING DATE: 1997-04-01 NUMBER OF SEQ ID NOS: 370 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NOS: 380 SEQ ID NOS: 380 SEQ ID NOS: 380 SEC ID 
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COATION: (35)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-08-764-846-141
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT2.2
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2.001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 141
LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 75.7%; Score 28; DB 10; Length 148; Similarity 50.0%; Pred. No. 90; 3; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 10; Length 138;
Pred. No. 85;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                     Sequence 298, Application US/09881752A Patent No. US20020115078A1 PAPERAL INFORMATION: APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 141, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
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illarity 66.7%;
Conservative
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ORGANISM: Homo sapiens
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Matches 4; Conserva
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Best Local Similarity
Matches 3; Conserv
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                                                                              75 COGVVC 80
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           1 CKGAIC 6
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US-09-881-752A-298
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GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Tomb, Jean Francois
APPLICANT: Tomb, Jean Francois
APPLICANT: Tomb, Generication of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in t
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
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                                                                                                                                                                                                                                                                         APPLICANT: SHERI L. BULJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5527.PC.01
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Patent No. US20020160456A1
                                                                                                                        GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
SHERI I., BULJK
ISA K. MUSHAHWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 38, Application US/08424550B Patent No. US20020119447Al GENERAL INFORMATION:
                                                                                JOHN N. SIMONS
TAMI J. PILOT-MATIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435435
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7. CORRESPONDENCE ADDRESS:
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                Score 29; DB 9; Length 188;
Pred. No. 74;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TOWNSDN, ROBERT
APPLICANT: TOWNSDN, ANDREW
TITLE OF INVENTION: AUTOMATED IDENTIFICATION OF PEPTIDES
FILE REFERENCE: 9195-064
CURRENT APPLICATION NUMBER: US/09/950,313
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.1
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APPLICANT: Glichrest, Barbara A.
APPLICANT: Glichrest, Barbara A.
APPLICANT: Glichrest, Barbara A.
APPLICANT: Taar, Mina
TITLE OF INVENTION: ALZHEIMER'S DISEASE
TITLE OF INVENTION: ALZHEIMER'S DISEASE
FILE REPRENCE: BU96-09A2
CURRENT APPLICATION NUMBER: US/09/866,898
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: PCT/US97/04966
PRIOR FILING DATE: 1997-03-28
PRIOR FILING DATE: 1997-03-28
PRIOR FILING DATE: 1997-03-28
           CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APLICATION NUMBER: 6/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER: OF SEQ ID NOS: 114
SEQ ID NO 109
LENGTH: 188
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US-09-950-313-6
US-09-950-313-6
Sequence 6, Application US/09950313
Patent No. US20020102610A1
GENERAL INFORMATION:
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Patent No. US20020051988Al
                                                                                                                                                                                                                                                                                                                           Query Match 78.4%;
Best Local Similarity 66.7%;
Matches 4; Conservative
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                                                                         ORGANISM: Rattus norvegicus
US-09-808-602-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.73
Matches 4; Conservative
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ORGANISM: Homo sapiens
US-09-950-313-6
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62 CSGSIC 67
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LENGTH: 760
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08;
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 523
LENGTH: 110
                                                                                                                                                                                                                              Query Match 75.7%; Score 28; DB 10; Length 10; Best Local Similarity 100.0%; Pred. No. 8.5; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 10; Length 110;
Pred. No. 70;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.7%; Score 28; DB 10; Length 58; 100.0%; Pred. No. 40; ative 0; Mismatches 0; Indels
                   NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Holloway, James L.
FILLE OF INVENTION: Human Chemokine
FILLE REFERENCE: 00-90
CURRENT APPLICATION NUMBER: US/09/970,108
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-925-302-523

Sequence 523, Application US/09925302

Patent No. US20020044941A1

; GENERAL INFORMATION:
                                                                                                                                                                    ; OTHER INFORMATION: CYClic peptide US-09-866-898-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/09970108
; Patent No. US20020091239A1
                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1996-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.7%;
Best Local Similarity 50.0%;
Matches 3; Conservative
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Best Local Similarity 100.1
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-970-108-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-925-302-523
                                                                                                                                                                                                                                                                                                                                                            6 KGAIC 10
                                                                                                                                                                                                                                                                                                                    2 KGAIC 6
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US-09-970-108-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 58
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                                                                                                                                              FEATURE:
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Sequence 109, Application US/09808602

Sequence 109, Application US/09808602

Sequence 109, Application US/09808602

SEXEMAL INFORMATION:

APPLICANT: Vernet, Corine A

APPLICANT: Herman, John L

APPLICANT: Mishra, Vishnu

APPLICANT: Mishra, Vishnu

APPLICANT: MacDougall, John

TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same
                                                                                                                                                                                                                                                           Xu, Tian Number of Internation (US20020127621A1el Family of Metalloproteases) NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FUKAN

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/871,388

FILING DATE: 31-May-2001

CLASSIFCATION NUMBER: 08/937,931

FILING DATE: CUNKNOWN>

NAME: OSMN RICHARD A

NAME: OSMN RICHARD A

NAME: OSMN RICHARD A

TELECOMUNICATION NUMBER: 35,627

REFERENCE/DOCKET NUMBER: 897-081

TELECOMUNICATION INCOMPATION:

TELECOMUNICATION INCOMPATION:

TELEFAX: (415) 343-4341

INFORMATION FOR EQ. 1D NO: 10:
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-871-388-10
                                                                                        Sequence 10, Application US/09871388; Patent No. US20020127621A1
GENERAL INFORMATION: APPLICANT: Rubin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                             Rooke, Jenny
Yavari, Reza
                                                                                                                                                                                         Pan, Duojia
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 CSGSIC 98
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                                                                    US-09-871-388-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Macina, Roberto
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Lu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Profile REFERENCE: DEX-0277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.4%; Score 29; DB 9; Length 84; 50.0%; Pred. No. 36; 1; Indels tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,997
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Patentin Version 3.1
EBOTH: 84
PRIOR APPLICATION NUMBER: 60/113,281
PRIOR FILING DATE: 1998-12-23
PRIOR FLILING DATE: 1998-12-23
PRIOR PRILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,283
PRIOR FILING DATE: 1998-12-23
PRIOR PRILING DATE: 1998-12-23
PRIOR PRILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-28
PRIOR FLILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATCHTIN VET: 2.0
SEQ ID NO 21
LENGTHENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 187, Application US/10001835 Patent No. US20020160387A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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CORGANISM: Homo sapien
US-10-001-835-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 CGGAIC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| :|
52 CRGVVC 57
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US-10-001-835-187
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(without alignments)
23.430 Million cell updates/sec
                                                                   November 9, 2002, 14:03:09; Search time 3.69231 Seconds
                                                                                                                                                                                                                                                                                                                                         92612
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          92612 seqs, 14418503 residues
                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                           US-09-632-748-10
37
                                                                                                                                             1 CKGAIC 6
                                                                                                                    Title:
Perfect score:
                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                             Sequence:
                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | | Sequence 12, Appl | , | Seguence 187, App | Sequence 10. Appl | 0 | ٩ | Section 4 acres 2 | , , | 523 | Sequence 208 | Segmence 141 App | An | - | Segmence 5784. An | Sequence 12780 A | Sequence 13105, 5 | Sequence 113 App | Secuence 6 April | |
|-----------|--------------------------|------|-------------------|------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-----------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|---------------------|---------------------|-------------------|------------------|-------------------|
| SUMMARIES | ID | | 02-03-8T2-C48-T7 | US-09-886-468-21 | US-10-001-835-187 | US-09-871-388-10 | US-09-808-602-109 | US-09-950-313-6 | US-09-866-898-4 | US-09-970-108-2 | US-09-925-302-523 | US-09-881-752A-298 | US-09-764-846-141 | US-08-424-550B-38 | US-09-895-913A-214 | US-09-815-242-5784 | US-09-815-242-12780 | US-09-815-242-13125 | US-09-808-602-113 | US-09-792-200B-6 | US-09-808-602-108 |
| | DB | ! 6 | 7 | 10 | σ | 10 | σ | 10 | 10 | 10 | 10 | 10 | 10 | | σ | 10 | 10 | 10 | σ | 10 | 6 |
| | Query
Match Length DB | | , ה
ה | T/R | 84 | 162 | 188 | 160 | 10 | 58 | 110 | 138 | 148 | 245 | 316 | 318 | 335 | 335 | 431 | 465 | 200 |
| о¥Р | Query
Match | 3 30 | 2 . | 81.1 | 78.4 | 78.4 | 78.4 | 78.4 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 | 75.7 |
| | Score | 33 | 9 (| 0 1 | 5 | 53 | 53 | 59 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 |
| | Result
No. | - | 1 (| 7 (| . | 4 | S | 9 | 7 | æ | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

| Sequence 112, App Sequence 114, App Sequence 363, App Sequence 70, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 54, Appl Sequence 54, Appl Sequence 50, Appl Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 52, Appli Sequence 54, Appli Sequence 54 | 174,
9, A |
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| 9 US-09-808-602-112
9 US-09-808-602-114
10 US-09-978-258-363
11 US-09-977-269-2
11 US-09-977-269-2
12 US-09-871-388-4
13 US-09-817-388-8
14 US-09-817-388-8
15 US-09-85-722-3
16 US-09-85-722-3
17 US-09-85-722-3
18 US-09-945-901-50
18 US-09-945-901-6
18 US-09-945-901-6
18 US-007-747-6
19 US-007-747-6
10 US-09-945-901-6
10 US-10-007-747-52 | 10 US-09-765-086-174
10 US-09-865-943-9 |
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| 7.857
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7.787 | 73.0 |
| \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ | 27 |
| 0112845678890113845678901138 | 44
45 |

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Aventis Pasteur Limited
TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses th
FILE REFERENCE: 77813-5
CURRENT APPLICATION NUMBER: US/09/886,468
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,280
PRIOR FILING DATE: 1998-12-23
## Second Process

| Sequence 1.2, Application US/09815248 |
| Sequence 1.2, Application US/09815248 |
| Patent No. US20020098540a1 |
| Patent No. US20020098540a1 |
| Patent No. US20020098540a1 |
| APPLICANT: RASTELL; LUCA |
| APPLICANT: PENNICA, DIACA |
| TILE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME |
| TILE REPERENCE: 10716.36 |
| CURRENT APPLICATION NUMBER: US/09/815,248 |
| CURRENT FILING DATE: 2001-08-20 |
| PRIOR FILING DATE: 2000-03-22 |
| NUMBER OF SEQ ID NOS: 38 |
| SEQTIANE: Patentin Ver. 2.1 |
| SEQ ID NO 12 |
| LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 12;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09886468 Patent No. US20020037293A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 86.5%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| :|
51 CKGGVC 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-815-248-12
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US-09-886-468-21
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1:1:11 78 CRGSIC 83

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; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBPDSXX US-10-270-837-20

; FEATURE:

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RESULT 15
US-10-270-837-2
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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        RESULT 14
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                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBPDSXX US-10-270-877-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBFDNLS US-10-270-837-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.8%; Score 31; DB 6; Length 616; 66.7%; Pred. No. 35; tive 2; Mismatches 0; Indels
  83.8%; Score 31; DB 6; Length 616; 66.7%; Pred. No. 35; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 6; Length 617;
Pred. No. 35;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/10270837
GENERAL INFORMATION:
APPLICANT: Saus, June
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD2
CURRENT APPLICATION NUMBER: US/10/270,837
CURRENT APPLICATION NUMBER: 09/212,563
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                  APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD1
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/270,877
CURRENT FILING DATE: 2002-10-11
PRIOR PEPLICATION NUMBER: 09/512,563
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION UNBER: 60/121,483
PRIOR APPLICATION UNBER: 60/121,483
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver: 2.0
LENGTH: 616
                                                                                                                                                                                                              Sequence 20, Application US/10270877 GENERAL INFORMATION:
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Best Local Similarity 66.77
Conservative
Query Match 83.8
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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78 CRGSIC 83
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78 CRGSIC 83
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US-10-270-877-20
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US-10-270-837-18
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US-10-270-877-18
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Pred. No. 35;
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TGS-01-174
Sequence 18, Application US/10270877
Sequence 18, Application US/10270877
GENERAL INFORMATION:
APPLICANT: Saus. Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD1
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512,563
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 617
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GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REPERENCE: 98.723.AD2
CURRENT APPLICATION UNMER: US/10/270,837
CURRENT FILING DATE: 2002-10-11
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PRIOR PILING DATE: 2002-10-11
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 199-02-24
PRIOR PILING DATE: 199-02-24
NUMBER OF SED ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
LENGTH: 624
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Best Local Similarity 66.70;
A: Conservative
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Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-270-837-2
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78 CRGSIC 83
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65 CRGSIC 70
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Pred. No. 34;
2; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD1
CURRENT APPLICATION NUMBER: US/10/270,877
CURRENT PILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512,563
FRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/121,483
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 8:
LENGTH: 598
US-10-270-837-12
Sequence 12, Application US/10270837
GENERAL INFORMATION:
APPLICATURY: Saus.
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-ADZ;
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512,563
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTING DATE: 1999-02-24
SOFTWARE: PATENTING DATE: 1995-02-24
SOFTWARE: PATENTING DATE: 1995-02-24
SOFTWARE: PATENTING DATE: 1995-02-24
SOFTWARE: PATENTING DATE: 1995-02-24
SEQ ID NO 12
LENGTH: 598
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TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD1
CURRENT APPLICATION NUMBER: US/10/270,877
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512,563
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Matches 4; Conservative 5
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Matches 4; Conserv
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65 CRGSIC 70
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US-10-270-877-12
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TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-401
FILE REFERENCE: 98-723-401
FURENT APPLICATION NUMBER: US/10/270,877
CURRENT FILING DATE: 2002-10-11
PRIOR PELLING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
SOFTWARE: PATENTION NUMBER: 60/121,483
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 12
LENGTH: 598
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Pred. No. 34;
2; Mismatches
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/121,483
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 598
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66.7%; Pred
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US-10-270-877-12
Sequence 12, Application US/10270877
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 66,/۱۳
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Best Local Similarity
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65 CRGSIC 70
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65 CRGSIC 70
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Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches
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65 CRGSIC 70
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78 CRGSIC 83
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US-10-270-837-10
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US-10-270-837-8
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                                                           ), OTHER INFORMATION: Description of Artificial Sequence: GPBPR3 US-10-270-877-16
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                                                                                                               Score 31; DB 6; Length 327;
Pred. No. 19;
2; Mismatches 0; Indels
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OTHER INFORMATION: Description of Artificial Sequence:
CHER INFORMATION: FLAG-GPBPDSXY/NLS
US-10-270-877-22
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TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD.
FILE REFERENCE: 98-723-AD.
FURENT APPLICATION NUMBER: 09/512,563
PRIOR APPLICATION NUMBER: 09/512,563
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 596
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TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-A01
CURRENT APPLICATION NUMBER: US/10/270,877
CURRENT FILING DATE: 2002-10-11
PRIOR PLILING DATE: 2000-02-24
PRIOR FILLING DATE: 2000-02-24
PRIOR FILLING DATE: 1999-02-24
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                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                     83.8%;
66.7%;
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Matches 4; Conservative
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78 CRGSIC 83
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78 CRGSIC 83
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US-10-270-877-22
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                                                                                                                       Query Match
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83.8%; Score 31; DB 6; Length 596;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Description of Artificial Sequence: Murine GPBP26 u_{\rm S}-10-270-837-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Human GPBP26 US-10-270-837-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.8%, Score 31; DB 6; Length 598;
66.7%; Pred. No. 34;
tive 2; Mismatches 0; Indels
0; Indels
                                                                                                                                                                                  Sequence 8, Application US/10270837
Sequence 8, Application US/10270837
GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD2
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512,563
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 6/121,483
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/10270837
GENERAL INFORMATION:
APPLICANT: Saus. Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/270,837
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512,563
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-24
NUMBER OF SED ID NOS: 63
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: 598
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Best Local Similarity 66./،
المالية 4; Conservative
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Best Local Similarity 66.74
Matches 4; Conservative
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Sequence 16, App]
Sequence 16, App]
                                                                                                                                   November 9, 2002, 14:01:49; Search time 2.53846 Seconds (without alignments) 26.619 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pending_Batents_AA_New:*

1: /cgn2_6/ptodata/2/paa_VCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa_VUSO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa_VUSO3_NEW_COMB.pep:*

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5: /cgn2_6/ptodata/2/paa_VUSO9_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa_VUSO3_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa_VUSO3_NEW_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                   39427 seqs, 11261862 residues
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                                                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum Match 1008
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                            Sequence:
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Appl Appli Appli Appli Appli Appli Sequence 10, Sequence 12, Sequence 22, Sequence 22, Sequence 8, Sequence 1 Sequence Sequence Sequence (Sequence Sequence Sequence Sequence Sequence Seguence Seguence Sequence US-09-513-999C-5046 US-09-513-999C-5047 US-10-270-877-12 US-10-270-837-20 US-10-270-877-20 US-10-270-837-18 US-10-270-837-18 US-10-270-837-10 US-10-270-837-12 US-10-270-837-2 US-10-270-837-4 US-10-270-837-6 US-10-270-837-6 US-10-270-877-6 US-10-270-837-24 US-10-270-877-4 Result No.

| Sequence 3471, App Sequence 363, App Sequence 14, Appli Sequence 6410, App Sequence 6410, Appli Sequence 6410, App Sequence 366, App | |
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| US-10-092-411A-3471
US-10-145-087A-363
US-10-145-087A-363
US-10-145-092A-363
US-10-162-522A-363
US-10-165-038A-363
US-10-175-038A-363
US-10-170-481A-363
US-10-145-088A-363
US-10-145-195A-363
US-10-145-195A-363
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66.7%; Pred. No. 19;
Live 2; Mismatches 0; Indels
                                                                       APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-402
FULE REPERENCE: 98-723-402
FULE REPERENCE: 98-723-402
CURRENT APPLICATION NUMBER: 09/512,563
PRIOR APPLICATION NUMBER: 60/121,483
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
SOFTWARE: PATENTION NUMBER: 60/121,483
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 16
LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/10270877

GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-Ab1
CURRENT APPLICATION NUMBER: US/10/270,877
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/121,483
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/121,483
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN PATE: 1999-02-24
SEQ ID NO: 52
SEQ ID NO: 53
SEQ ID NO: 53
LENGTH: 327
US-10-270-837-16
Sequence 16, Application US/10270837
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 83.8
Best Local Similarity 66.7
Matches 4; Conservative
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78 CRGSIC 83
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US-10-270-837-16
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83.3%; Pred. No. 36;
tive 0; Mismatches
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                                                          5; Conservative
                  Best Local Similarity
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A; Residues: 1-65 <BUL>
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A; Reference number: 218456
A; Accession: T16073
A; Accession: T16073
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary;
A; Residues: 1-975 <GEI>A; CGEI>A; CGEI>A; CGEI>A; CROSS-references: EMBL:028737; NID:g860717; PID:g860722; PIDN:AAA68275.1; CESP:F14B8.5
A; Experimental source: strain Bristol N2
C; Genetics: A; Gene: CESP:F14B8.5
A; Gene: CESP:F14B8.5
A; Introns: 48/2; 84/2; 114/1; 191/2; 227/3; 291/2; 308/2; 325/3; 350/3; 383/2; 416/2; 48
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.X.; Liu
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C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-May-1997

C;Accession: S65712

B;Saito, S.; Huzaiker, P.E.

Biochim. Biophys. Acta 1289, 65-70, 1996

A;Title: Differential sensitivity of metallothionein-1 and -2 in liver of zinc-injected A;Accession: S65712; MUID:96195842; PMID:8605234

A;Status: preliminary
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A;Residues: 1-1617 <STO>
A;Cross_references: GB:AE005172; NID:g6598587; PIDN:AAF18642.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein F5J5.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.1%; Score 30; DB 2; Length 52;
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A,Residues: 1.23;24.46;47.52 <SAI>
C;Superfamily: metallothionein
C;Reywords: blocked amino end
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Best Local Similarity 83.3
Matches 5; Conservative
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C; Species: Methanococcus jannaschil
C; Species: Methanococcus jannaschil
C; Date: 13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change 21-Jul-2000
C; Accession: H64324
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Reference number: A64300; MuID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U67476; GB:L77117; NID:g1590942; PIDN:AAB98183.1; PID:g1590944 C;Genetics:
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A; Start codon: GTG
C; Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
C; Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
F; 6-63/Domain: ferredoxin 2[4Fe-4S] homology <FER>
F; 13, 18, 21, 55/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F; 25, 45, 48, 51/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
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Gaps
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1; Indels
                                                                                                                                                                                                                                                                                                                                                                          ferredoxin 2[4Fe-4S] - Methanococcus jannaschii
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Local Similarity 66.7 les 4; Conservative
                                                                                                                                          fertillin beta chain - human
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A;Gene: CESP:B0024.14
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127 CRGSIC 132
     540 CRGSIC 545
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                                                                                                                                                                                                                                                                                                                                                                   Jebobs dehydrogenase (EC 1.-.-.) [similarity] - Arabidopsis thaliana alcohol dehydrogenase (EC 1.-.-.) [similarity] - Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: D86357
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; J.H.; Li, X.; Lin, X.; Liu, Z.A.; Luros, J.S.; Majti, E.; Kim, C.C.C., Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Lu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakao, H.
Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: D86357
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.388 <STO>
A; Residues: 1.388 <STO>
A; Cross-references: GB: AE005172; NID: 96587845; PIDN: AAF18534.1; GSPDB: GN00141
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modulin-like protein [imported] - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear crees)

C;Species: Arabidopsis thaliana (mouse-ear crees)

C;Species: Arabidopsis thaliana (mouse-ear crees)

C;Accession: T51805

C;Accession: T51805

A;Ed;Accession: T51805

A;Title: The Lotus japonicus LjNOD70 nodulin gene encodes a protein with similarities to A;Title: The Lotus japonicus LjNOD70 nodulin gene encodes a protein with similarities to A;Title: The Lotus japonicus LjNOD70 nodulin gene encodes a protein with similarities to A;Accession: T51805

A;Accession: T51805

A;Accession: T51805

A;Molecule type: mRNA

A;Molecule type: mRNA

A;Residues: 1-559 <SZC>
A;Cross-references: EMBL:AP031244; PIDN:AAC39501.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C; Keywords: oxidoreductase; zinc
F; 53, 76, 185/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
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                                                                                    Length 295;
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                                                                                                                                          0; Indels
                                                                               83.8%; Score 31; DB 2;
66.7%; Pred. No. 90;
tive 2; Mismatches
A;Gene: APE2344
C;Superfamily: lipoic acid synthase
                                                  Ouery Match
Best Local Similarity 66./*,
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Best Local Similarity
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Matches 4; Conserva
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C; Accession: JC4861
R; Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A; Title: Molecular cloning of the human fertilin beta subunit.
A; Reference number: JC4861; MUID:96295488; PMID:8702389
A; Accession: JC4861
A; Molecule type: mRNA
A; Residues: 1-734 <GUDA
A; Residues: 1-734 <GUDA
A; Rocoment: This protein is an integral sperm membrane glycoprotein, and plays a role C; Comment: This protein is an integral beam membrane protein
C; Superfamily: mouse meltrin alpha; disintegrin homology
C; Superfamily: mous
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A;Introns: 46/3; 84/1; 212/1; 307/2; 345/2; 394/1; 424/2; 481/1; 596/1; 702/1; 765/3;
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Secession: T18649
R;McMurray, A.
submitted to the EMBL Data Library, April 1996
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16073
C;Species: Homo sapiens (man)
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jan-2000
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66.7%; Pred. No. 2.2e+02;
live 2; Mismatches 0; Indels
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submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F14B8.
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A;Accession: T18649
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-884 <WILL>
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A; Experimental source: clone B0024
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ribosomal protein L32 TC0195 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydla muridarum, Chlamydia trachomatis MoPn
C;Access: Chlamydla muridarum, Chlamydia trachomatis MoPn
C;Accession: H81730
C;Accession: H81730
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C; Dodson, R; Gwinn, M; Nelson, W; DeBoy, R.; Kolonay, J.; White, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUD:20150255; PMID:10684935
A;Accession: H8170
A;Acce
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: E72462
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339; PMID:10382966
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A;Ressidues: 1-295 <KAM>
A;Crossreferences: DDBJ:AP000064; NID:g5105945; PIDN:BAA81357.1; PID:g5106046
A;Experimental source: strain Kl
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: probable aquaporin
C;Species: Beta vulgaris (beet)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C;Accession: T14600
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Pred. No. 25;
1; Mismatches 1; Indels
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A; Molecule type: mRNA
A; Residues: 1-281 <QIX>
A; Cross-references: EMBL: U60148; NID: 91402834; PID: 91402835
A; Experimental source: strain Detroit dark red
C; Superfamily: lens fiber membrane major intrinsic protein
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submitted to the EMBL Data Library, June 1996
X:Reference number: 2.18157
A;Accession: T14600
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Pred. No.
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                             probable electron transfer protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Diana, Bisho, Siao, Y.
Scession: C64890
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Recession: C64890
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Accession: C64890
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-356 CBLAP
A;Cross-references: GB:AE000236; GB:U00096; NID:g1787652; PIDN:AAC74474.1; PID:g1787658;
A;Cross-references: Strain K-12, substrain Mg1652; PiDN:AAC74474.1; PID:g1787658;
A;Experimental source: strain K-12, substrain Mg1652; Cytochrome-b5 reductase homology; ferred
C;Superfamilly: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred
C;Superfamilly: ferredoxin [2Pe-25; electron transfer: iron-sulfur protein; metalloprotein; transmembran
F;116-132/Domain: ferredoxin [2Pe-25] homology 
F;299,304,307,337/Binding site: 2Fe-25 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Gallione, C.J.; Rose, J.K.
J. Virol. 46, 162-169, 1983
A;Title: Nucleotide sequence of a cDNA clone encoding the entire glycoprotein from the
A;Reference number: A04118; MUID:83138980; PMID:6298453
A;Accession: A04118
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C,Species: vesicular stomatitis New Jersey virus
C,Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-517/Product: spike glycoprotein G #status predicted <SIG>
F;23-517/Product: spike glycoprotein G #status predicted <SIG>
F;473-489/Domain: transmembrane #status predicted <TMN>
F;179,340/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 1-517 cGAL>
A;Cross-references: GB:V01214; NID:g61839; PIDN:CAA24525.1; PID:g61840
C;Genetics:
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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 9, 2002, 13:59:34; Search time 8.30769 Seconds (without alignments) 69.430 Million cell updates/sec Run on:

US-09-632-748-10 37 Title: Perfect score:

1 CKGAIC 6 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Author Description 33 89.2 626 2 55209 34 89.2 656 2 55209 35 86.5 356 2 664890 31 83.8 295 2 7514600 31 83.8 295 2 7514600 31 83.8 295 2 7514600 31 83.8 295 2 7514600 31 83.8 295 2 7514600 31 83.8 295 2 7514600 31 83.8 295 2 7514600 31 83.8 84 2 718649 32 81.1 52 2 565712 33 81.1 124 2 718649 34 81.1 124 2 718649 35 81.1 124 2 718649 36 81.1 124 2 718649 37 81.1 124 2 718649 38 81.1 124 2 718649 39 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 124 2 718649 30 81.1 128 2 7109817 30 81.1 28 2 712434 30 81.1 284 2 712434 30 81.1 284 2 712434 30 81.1 284 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 30 81.1 285 2 712435 | | | æ | | | SUPPLEATES | |
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| 30 81.1 130 2 F72120 probable ferredo 81.1 130 2 D86501 probable ferredo 130 81.1 130 2 D86501 probable water of 2 T09817 probable water of 2 T09817 probable water of 2 T09796 probable water of 2 T09796 probable water of 2 T09796 probable membrane 30 81.1 280 2 T05780 plasma membrane 30 81.1 280 2 T05780 plasma membrane 30 81.1 281 2 T09124 probable aquapor 30 81.1 284 2 T12434 probable plasma 130 81.1 284 2 T12557 aquaporin NT2 - 30 81.1 285 2 T12435 probable plasma 30 81.1 285 2 T12435 probable plasma 30 81.1 285 2 T12435 probable plasma 30 81.1 285 2 T12435 | ، و | 30 | 81.1 | 124 | ~ | AG3252 | hypothetical cytos |
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| 30 81.1 187 2 T09817 probable water of a frought-induced 30 81.1 216 2 T04368 plasma membrane 30 81.1 278 2 A84545 plasma membrane 30 81.1 280 2 T05780 plasma membrane 30 81.1 281 2 T05780 plasma membrane 30 81.1 281 2 T12434 probable aquapor 30 81.1 284 2 T1257 aquapor 30 81.1 284 2 T1257 aquapor 30 81.1 285 2 T12342 major intrinsic 30 81.1 285 2 T12435 probable plasma 30 81.1 285 2 T12435 | œ : | 30 | 81.1 | 130 | N | D86501 | |
| 30 81.1 198 2 709796 drought-induced 30 81.1 276 2 704368 plasma membrane 30 81.1 278 2 705780 plasma membrane 30 81.1 280 2 705780 plasma membrane 30 81.1 281 2 709124 probable aquapor 30 81.1 284 2 712557 mipE protein - c 30 81.1 284 2 712374 major intrinsic 30 81.1 285 2 712435 probable plasma 30 81.1 285 2 712435 probable plasma | σ, | 30 | 81.1 | 187 | 7 | T09817 | probable water cha |
| 30 81.1 216 2 704368 plasma membrane 30 81.1 278 2 A84545 hypothetical prophane 30 81.1 280 2 709124 probable aquapor 30 81.1 281 2 712434 probable plasma 30 81.1 284 2 712557 mipE protein - c 30 81.1 284 2 712342 aquaporin NT2 - 30 81.1 285 2 712342 major intrinsic 30 81.1 285 2 712435 probable plasma | ٠, | 30 | 81.1 | 198 | ~ | T09796 | drought-induced ma |
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| 30 81.1 280 2 T05780 plasma membrane 30 81.1 281 2 T09124 probable aquapor 30 81.1 283 2 T12434 probable aquapor 30 81.1 284 2 T12557 mipE protein - c 30 81.1 284 2 T03794 aquaporin NT2 - 30 81.1 285 2 T12435 probable plasma 30 81.1 285 2 T12435 | ~ | 30 | 81.1 | 278 | 7 | A84545 | hypothetical prote |
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30 81.1 285 2 T12435 probable plasma | S | 30 | Н | 283 | 7 | 13 | probable plasma me |
| 30 81.1 284 2 T03794 aquaporin NT2 -
30 81.1 285 2 T12342 major intrinsic
30 81.1 285 2 T12435 probable plasma | 9 | 30 | 81.1 | 284 | 7 | 10 | protein - c |
| 30 81.1 285 2 T12342 major intrinsic
30 81.1 285 2 T12435 probable plasma | 7 | 30 | | 284 | 7 | 9 | orin NT2 - |
| 30 81.1 285 2 T12435 probable plasma | æ (| 30 | 81.1 | 282 | ~ | - | ic |
| | on. | 30 | 81.1 | 285 | 7 | 24 | plasma |

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|-----------------------------------------------|------------------|---------|--------|------|--------------------------------------------------------------------------------------------------------------|--------------------|
| 30 | 30 | 81.1 | 282 | ~ | S44085 | plasma membrane in |
| 31 | 30 | 81.1 | 282 | ~ | T06434 | plasma membrane in |
| 32 | 30 | 81.1 | 285 | 7 | D84789 | hypothetical prote |
| 33 | 30 | 81.1 | 285 | ~ | E84789 | hypothetical prote |
| 34 | 30 | 81.1 | 286 | ~ | T47935 | plasma membrane in |
| 35 | 30 | 81.1 | 286 | ~ | T14601 | plasma membrane ma |
| 36 | 30 | 81.1 | 286 | ~ | T04367 | plasma membrane in |
| 37 | 30 | 81.1 | 286 | ~ | S42542 | ripening-associate |
| 38 | 30 | 81.1 | 286 | 2 | T02451 | plasma membrane in |
| 39 | 30 | 81.1 | 286 | ~ | T06738 | probable plasma me |
| 40 | 30 | 81.1 | 286 | 7 | A86147 | hypothetical prote |
| 41 | 30 | 81.1 | 287 | 7 | T09791 | drought-induced ma |
| 42 | 30 | 81.1 | 287 | 7 | T12440 | mipC protein - com |
| 43 | 30 | 81.1 | 287 | 7 | T05378 | probable plasma me |
| 44 | 30 | 81.1 | 287 | 0 | S44084 | plasma membrane in |
| 45 | 30 | 81.1 | 287 | 7 | S60455 | transmembrane prot |
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| | | | | | ALIGNMENTS | |
| RESULT 1
S52209 | | | | | | |
| noncapsid protein NS1 N; Alternate names: non | protei
e name | n NS1 - | muscor | vy (| noncapsid protein NS1 - muscovy duck parvovirus
N;Alternate names: nonstructural protein NS1; NS1 protein | |

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Apporthetical protein BMEI1871 [imported] - Brucella melitensis (strain 16M)
C; Species: Brucella melitensis
C; Date: Dreb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Accession: Al3485
R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
A; Reference number: AD3252; PMID:11756688
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-245 < KUR>
A; Residues: 1-245 < KUR>
A; Residues: 1-245 < KUR>
A; Cross-references: GB: AE008917; PIDN: AAL53052.1; PID:g17983912; GSPDB: GN00190
A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
N'Alternate names: nonstructural protein NS1; NS1 protein
C'Species: muscovy duck parvovinus
C'Date: 19-War-1997 #sequence_revision 19-War-1997 #text_change 26-Aug-1999
C'Accession: S5209
R'Addorl, Z.; Brdel, J.; Nagy, J.; Kisari, J.
R'Addorl, Z.; Brdel, J.; Nagy, J.; Kisari, J.
A;Reference number: S5209
A;Reference number: S5209
A;Recession: S5209
A;Recision: S5209
A;Recision: S5209
A;Residues: 1-626 <ZAD>
A;Residues: 1-626 <ZAD>
A;Cross-references: EMBL:X75093; NID:g609091; PIDN:CAA52983.1; PID:g609092
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: NS1
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 CKGSVC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKGAIC 6
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Matches
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A:Gene: BMEI1871

A; Map position: I

Score 32; DB 2; Length 245; Pred. No. 50; 86.5%; Best Local Similarity Query Match

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KW Transport; Transmembrane; Multigene family.
SQ SEQUENCE 285 AA; 30429 MW; D51213A68EEBB508 CRC64;
Query Match 81.1%; Score 30; DB 1; Length 285;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 CKGAIC 6 | | | | | | | Db 131 CLGAIC 136

Search completed: November 9, 2002, 14:01:46 Job time : 6.61538 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. Columbia; MEDINIA: MEDINIA: MEDINIA: Columbia; MEDINIAE-20083487; PubMed-10617197; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Ee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
   VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: WATER CHANNEL PROTEIN IN PLASMA MEMBRANE.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Landsberg erecta; TISSUE=Root;
MEDLINE-95004661; PubMed=7920711;
Kammerloher W., Fischer U., Plechottka G.P., Schaeffner A.R.;
"Water channels in the plant plasma membrane cloned by immunoselection from a mammalian expression system.";
Plant J. 6:187-199(1994).
                                                                             Score 30; DB 1; Length 119;
                                                                                                                     1; Indels
                   BY SIMILARITY.
: 229241793FA826F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transport; Transmembrane; Multigene family.
CONFLICT 141 143 VKA -> RQS (IN REF. 1).
                                                                                                                                                                                                                                                                                                      P43287; 095KR8;
01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-Basma membrane intrinsic protein 2B.
PIP2B OR A72G37170 OR T2N18.7.
                                                                                                                                                                                                                                                                                          PRT; 285 AA,
                                                                                               Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000425; MIP_family. Pfam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00783; MINTRINSICP.
PRODOM; PD000295; MIP_family; 1.
TIGREAMS; TIGRO0861; MIP; 1.
PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC006260; AAD18142.1; -. HSSP; P29972; 1H61.
32 32 v
49 49 E
119 AA; 12856 MW;
                                                                         81.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X75884; CAA53478.1;
                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                           85 CKGFVC 90
                                                                                                                                                       1 CKGAIC 6
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                                                                                                                                                                                                                                                                                          WC2B_ARATH
                   CA_BIND
SEQUENCE
                                                                             Query Match
 CA_BIND
                                                                                                                                                                                                                                                RESULT 14
WC2B_ARATH
                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Plasma membrane intrinsic protein 2C (Water-stress induced tonoplast intrinsic protein) (WSI-TIP).
PIP2C OR RD28 OR AT2G37180 OR T2N18.6.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Yamaquchi-Shinozaki K., Koizumi M., Urao S., Shinozaki K.;
"Molecular cloning and characterization of 9 cDNAs for genes that are responsive to desiccation in Arabidopsis thaliana: sequence analysis of one cDNA clone that encodes a putative transmembrane channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20083487; PubMed=10617197; MEDLINE-20083487; PubMed=10617197; Lin X.; Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Lin X.; Kaul S., Rounsley S.D., Shea T.P., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Diayam L., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                         ;;
0
                                                    81.1%; Score 30; DB 1; Length 285; 83.3%; Pred. No. 48;
                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 234 A -> S (IN REF. 1).
285 AA; 30453 MW; 04364AFE7531EE10 CRC64;
                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Cell Physiol. 33:217-224(1992)
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00783; MINTRINSICP.
PRODON; PD0000285; MIP_family; 1.
TIGRPAMS; TIGRO0861; MIP; 1.
PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AC006260; AAD18141.1; -.
HSSP; P29972; 1H61.
InterPro; IPR000425; MIP_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D13254; BAA02520.1; -.
                                 Query Match
Best Local Similarity 83...
5, Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00230; MIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                             131 CLGAIC 136
                                                                                                                         1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                                                     WC2C_ARATH
P30302;
CONFLICT
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                                                                                                                                                                                                                 RESULT 15
WC2C_ARATH
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or send an email to license@isb-sib.ch).
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STRAIN-JAL-1/ DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Doughberty B.A., Tomb J.-F., Adams M.D., Ratch C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.W., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
-1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                   MISSING (IN REF. 2).

D -> H (IN REF. 2).

V -> G (IN REF. 3).

V -> G (IN REF. 3).

V -> A (IN REF. 2).

H -> D (IN REF. 2).

H -> D (IN REF. 2).

G -> S (IN REF. 3).

EEC -> DEF (IN REF. 3).

G -> S (IN REF. 3).

G -> S (IN REF. 3).

D -> Y (IN REF. 3).

N -> D (IN REF. 3).
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BBF27B8BEC7F92D3 CRC64;
     N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative ferredoxin MJ0199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.8%; Score 31; DB
66.7%; Pred. No. 69;
tive 1; Mismatches
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Pfam; PF00037; fer4; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82466 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Best Local Similarity
4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 CSGAVC 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FERA_METJA
AC 057652;
DT 01-NOV-1997
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VIA CARBONYL OXYGEN (BY SIMILARITY).
VIA CARBONYL OXYGEN (BY SIMILARITY).
                                                                     SIMILARITY)
                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                     2-acylhydrolase).
Acanthophis antarcticus (Common death adder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Acanthophis.
NCBI_TaxID=8605;
                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 (EC 3.1.1.4) (Acanthin I) (Phosphatidylcholine
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVITY.

--- CAPALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.

--- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

--- SUBCELLULAR LOCATION: Secreted.

--- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
Hypothetical protein; Electron transport; Iron-sulfur; 4Fe-4S;
                                                                                                                                           Score 30; DB 1; Length 62;
Pred. No. 13;
                                                                                                                                                                     1; Indels
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                                 IRON-SULFUR 1 (4FE-4S) (1

IRON-SULFUR 1 (4FE-4S) (1

IRON-SULFUR 1 (4FE-4S) (1

IRON-SULFUR 2 (4FE-4S) (2

IRON-SULFUR 2 (4FE-4S) (2

IRON-SULFUR 2 (4FE-4S) (1
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                                                                                                                                                                    0; Mismatches
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Pram; PF00066; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000389; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Calcium; 1
                                                                                                                                               81.1%;
83.3%;
                                   10
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6650 MW;
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93
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                                                                                                                                                         Local Similarity
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                          Complete proteome.
                                                                                                                                                                                                                10 CKGAEC 15
                                                                                                                                                                                           1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Venom;
                                                                                                                                                                                                                                                                     PA21_ACAAN
P81236;
                                                                             METAL
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SEQUENCE
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vidaeus C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADOZ_HUMAN STANDARD; PRT; /35 An. 099965; P78126; 30-MAZ-2000 (Rel. 39, Created) 30-MAZ-2000 (Rel. 39, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) ADAM 2 precursor (A disintegrin and metalloproteinase domain 2) (Fertilin beta subunit) (PH-30) (PH30).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gupta S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F., "Molecular cloning of the human fertilin beta subunit."; Biochem. Biophys. Res. Commun. 224:318-326(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human fertilin beta: identification, characterization, and chromosomal mapping of an ADAM gene family member."; Mol. Reprod. Dev. 46:363-369(1997).
                                                                                                                                                                                                                                                                                                                                                                                                            83.8%; Score 31; DB 1; Length 624; 66.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                             371 396 MISSING (IN ISOFORM 2).
624 AA; 71111 MW; FD708AFFB25FCD31 CRC64;
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                                                                                                                                                               InterPro; IPR001849; PH.
InterPro; IPR002913; START.
Fram; PF01852; START; 1.
SMART; SM00233; PH; 1.
SMART; SM00234; START; 1.
SMART; SF50043; PH_DOMAIN; 1.
PROSITE; PS50048; START; 1.
Transferase; Coiled coil; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Testis;
MEDLINE-96295488; PubMed-8702389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Testis;
MEDLINE=97224507; PubMed=9070941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97193554; PubMed=9041139;
                                                                                                       EMBL; AF232932; AAG42048.1; -.
EMBL; AF232934; AAG42050.1; -.
EMBL; AK012989; BAB28581.1; -.
                                                                                                                                                     MGD; MGI:1915268; Col4a3bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene (FTNB).";
Genomics 40:190-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                117
303
618
396
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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65 CRGSIC 70
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                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
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                                                                                                                                                                                                                                                                                                                  DOMAIN
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AD02_HUMAN
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CHINGTION: SPERM SURFACE MEMBRANE PROTEIN THAT MAY BE INVOLVED IN SPERM-EGG PLASMA MEMBRANE ADHESION AND FUSION DORING FRETILIZATION. COULD HAVE A DIRECT ROLE IN SPERM-ZONA BINDING OR MIGRATION OF SPERM FROM THE UTERUS INTO THE OVIDUCT. INTERACTIONS WITH EGG MEMBRANE COULD BE MEDIATED VIA BINDING BETWEEN ITS DISINITESTIN-LIKE DOMAIN TO ONE OR MORE INTEGRINS RECEPTORS ON THE EGG. : SIBCELLULAR LOCATION: Type I membrane protein.

1. TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN SPERMATOGENIC CELLS IN THE SEMINITESTOUS CELLS. NOT DETECTED IN FETAL TISSUES.

2. IN THE SEMINITESTOUS CELLS. NOT DETECTED IN FETAL TISSUES.

2. IN THE SEMINITESTOUS CELLS. NOT DETECTED IN FETAL TISSUES.

3. DOMAIN COULD BE INVOLVED IN THE BINDING TO EGG INTEGRIN RECEPTOR DOMAIN COULD BE INVOLVED IN THE BINDING.

3. IN THE SIGNAL AND THE METALLOPROTEASE DOWAIN ARE CLEAVED DURING THE SPIRAL PROTEIN RECEPTOR SET AND THE SIGNAL AND THE METALLOPROTEASE DOWAIN ARE CLEAVED DURING THE SPIRAL SHAWALS, EXISTS AS A HETERODIMER COMPOSED OF AN ALPHA AND BETA SUBBUITAS: IN HUMAN, FERFILLIN ALPHA IS A PSEUDOGENE.

3. SIMILARITY: CONTAINS I EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001762; Disintegrin.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001561; EGF-11ke.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR00130; Zn_MTpeptdse.
R PFam; PF001200; disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
R Pfam; PF01421; Reprolysin; 1.
R Pfam; PF01422; Pep_M12B_propep; 1.
R PRIMTS; PR00289; DISINTEGRIN.
R PROMITS; PS00164; DISINTEGRIN.
R PROSITE; PS00125; ADAM_MEPRO; 1.
R PROSITE; PS00127; DISINTEGRIN_1: 1.
R PROSITE; PS00127; DISINTEGRIN_1: 1.
R PROSITE; PS01186; EGF_1; FALSE_NEG.
R PROSITE; PS01186; EGF_2; FALSE_NEG.
R PROSITE; PS01186; EGF_2; FALSE_NEG.
R PROSITE; PS01184; ZINC_PR0TEARE; FALSE_NEG.
R PROSITE; PS01184; ZINC_PROTEARE; FALSE_NEG.
R PROSITE; PS01184; ZINC_PROTEARE; FALSE_NEG.
R PROSITE; PS01184; ZINC_PROTEARE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
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BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U52370; AAC51110.1; -. EMBL; U38805; AAD04206.1; -. EMBL; X99374; CAA67753.1; -. HSSP; P17494; IKST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; M12.950; -.
Genew; HGNC:198; ADAM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Glycoprotein;
SIGNAL 116
PROPEP 17 174
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DISULFID
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=20568301; Pubmed=11007769;
MEDLINE=20568301; Pubmed=11007769;
Valety A., Revert-Ros F., Martinez-Martinez P., Navarro S., Rosello E., Viettes B., Granero F., Forteza J., Saus J.;
"Goodpasture antigen-binding protein, the kinase that phosphorylates the Goodpasture antigen, is an alternatively spliced variant implicated in autoimmune pathogenesis.";
J. Biol. Chem. 275:40392-40399(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Phosphorylates on Ser and Thr residues the Goodpasture autoantigen (in vitro). Isoform 2 seems to be less active.

-!-CMTALTYTC ACTIVITY: AFP + a protein = ADP + a phosphoprotein.
-!-SUBLUTY: Interacts with COL4A3.
-!-SUBCULTY: Interacts with COL4A3.
-!-SUBCULTY: Interacts with COL4A3.
-!-ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta26/GBBDD56; are produced by alternative splicing.
-!-TISSUE SPECIFICITY: Widely expressed.
-!-SIMILARITY: CONTAINS 1 PH DOMAIN.
-!-SIMILARITY: CONTAINS 1 START DOMAIN.
                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
600dpasture antigen-binding protein (EC 2.7.1.37) (GPBP) (Collagen type IV alpha 3 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raya A., Revert F., Navarro S., Saus J.;
Characterization of a novel type of Serine/Threonine kinase that
specifically phosphorylates the human goodpasture antigen.";
J. Biol. Chem. 274:12642-12649(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
MEDLINE-99230287; PubMed-10212244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Coiled coil; Alternative splicing.
                                                                                                                                                                                                                                                 624 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF136450; AAD30288.1; -. EMBL; AF232930; AAG42046.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC000102; AAH00102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 604677; -.
InterPro; IPR001849; PH.
InterPro; IPR002913; START.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC: 2205; COL4A3BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00169; PH; 1.
Pfam; PF01852; START; 1.
SMART; SM00233; PH; 1.
SMART; SM00234; START; 1.
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                             C43B_HUMAN
Q9Y5P4; Q9H2S8;
                                                                    65 CRGSIC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COL4A3BP.
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C43B_HUMAN
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REAUTOLINE-TOOLOGE FROM N.A. (ISOFORM 2).

REQUENCE FROM N.A. (ISOFORM 2).

REQUENCE TROBSEGE, bubmed=11217851;

REDINE-21085660; Dubmed=11217851;

RA Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa T., Saito R.,

RA Gaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Brownstein M.J., Bult C., Fletcher C., Flujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Flujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Ringwald M., Ramiya M., Lee N.H.,

RA Brownstein M.J., Mashima J., Mashama J., Maszarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sazaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y.,

RA Hayashizaki Y.,

RA Floricional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raya A., Revert-Ros F., Martinez-Martinez P., Navarro S., Rosello E., Vieltes B., Granero F., Forteza J., Saus J.;
"Goodpasture antigen-binding protein, the kinase that phosphorylates the Goodpasture antigen, is an alternatively spliced variant implicated in autoimmune pathogenesis.";
J. Biol. Chem. 275:40392-40399(2000).
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i - FUNCTION: Phosphorylates on Ser and Thr residues the Goodpasture
                                                                                                                                                                                                                                                                                                                                                       Q9EQG9; Q9EQG8;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Goodpasture antigen-blunding protein (EC 2.7.1.37) (GPBP) (Collagen type IV alpha 3 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoantigen (in vitro). Isoform 2 seems to be less active (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2/Delta26/GPBPD26; are produced by alternative splicing.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 START DOMAIN.
                                                                                                                    DB 1; Length 624;
                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Interacts with COL4A3.
                                                         MISSING (IN ISOFORM 2).
A125162492AC5A0E CRC64;
                  COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                         Pred. No. 60;
2; Mismatches
                                                                                                                    Score 31;
                                          START
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20568301; PubMed=11007769;
117 PH
303 CO
618 ST
396 MI
                                                                                                                        83.88;
                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
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  23
263
389
6371
624 AA;
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                           |:|:||
65 CRGSIC 70
                                                                                                                                                                                                  1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                         C43B MOUSE
                                          DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COL4A3BP.
                                                                                 SEQUENCE
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                  RESULT 10
C43B_MOUSE
                                                                                                                                                               Matches
    REFFE
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                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagazi Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; T., Kubota K., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an acrobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl."; DNA Res. 6:83-104[1999].
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Lipoate biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable lipoic acid synthetase (LIP-SIN) (Lipoate synthase).
                                                                                                                                                                                                                   83.8%; Score 31; DB 1; Length 282; 83.3%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON-SULFUR (POTENTIAL).
2FB10A1A13F4DBFB CRC64;
                                                           DIST, PESTIN, PEROUGAS; MID_family.
Pfam; PR00230; MIP; 1.
PRINTS; PR00783; MINFISTOR.
PRODOM: PD000295; MIP_family; 1.
TIGRPAMS; TIGRO0861; MIP; 1.
PROSTIE; PS00221; MIP; 1.
PROSTIE; PS00221; MIP; 1.
SEQUENCE 282 AA; 30260 MW; 42AA96F0EB0F1444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON-SULFUR (POTENTIAL). IRON-SULFUR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             295 AA.
                                                                                                                                                                                                                                 83.3%; Pred. no.
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003698; Lipoate_synth.
Pfam; PF02546; Lipoate_synth; 1.
TIGRPAMS; TIGR00510; lipA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iron-sulfur; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP000064; BAA81357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 67 I
295 AA; 32435 MW;
                            EMBL; U18403; AAA86991.1; -. HSSP; P29972; 1H6I.
                                                                                                                                                                                                                                         Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPA OR APE2344.
                                                                                                                                                                                                                                                                                                                        128 CAGAIC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                          1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                             LIPA_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY
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                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=20568301; PubMed=11007769;
Raya A., Revert-Ros F., Martinez-Martinez P., Navarro S., Rosello E., Vieites B., Granero F., Forteza J., Saus J.;
Goodpasture antigen-binding protein, the kinase that phosphorylates the Goodpasture antigen, is an alternatively spliced variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    implicated in autoimmune pathogenesis.";
J. Biol. Chem. 275:40392-40399(2000).
-i- FUNCTION: Phosphorylates on Ser and Thr residues the Goodpasture autoantigen (in vitro). Isoform 2 seems to be less active (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                              Gaps
                                                                                                                                                                                                      C43B_BOVIN STANDARD; PRT; 624 AA.
OGGKT7, OGGKI6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Goodpasture antigen binding protein (EC 2.7.1.37) (GPBP) (Collagen type IV alpha 3 binding protein).
                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Bukaryota; Metazooa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
-:- SUBUNIT: Interacts with COL4A3.
-:- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta26/GPBPD26; are produced by alternative splicing.
-:- SIMILARITY: CONTAINS 1 PH DOMAIN.
-:- SIMILARITY: CONTAINS 1 START DOMAIN.
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           83.8%; Score 31; DB 1; Length 295; 66.7%; Pred. No. 32;
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490D7FD950195476 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Coiled coil; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 60;
2; Mismatches
                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50003; PH DOMAIN; 1. PROSITE; PS50848; START; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF232931; AAG42047.1; -. EMBL; AF232933; AAG42049.1; -.
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InterPro; IPR002913; START.
Ouery Match
Best Local Similarity 66.۰۰
امر 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00169; PH; 1.
Pfam; PF01852; START; 1.
SMART; SMO0233; PH; 1.
SMART; SMO0234; START; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   624 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                     34 CEGALC 39
                                                                                  1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                COL4A3BP.
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                                                                                                                                                                                                                                                                                                                                                              Gallione C.J., Rose J.K.;

"Nuclectide sequence of a cDNA clone encoding the entire glycoprotein from the New Jersey serotype of vesicular stomatitis virus.";

J. Virol. 46.162-169(1983).

-I- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.

IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS BY THE CELL.

THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRON

AND THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLABUNIC

FACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                   Vesicular stomatitis virus (serotype New Jersey / strain Ogden).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Vesiculovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPIKE GLYCOPROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
A5F0B008B3490194 CRC64;
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      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001903; Rhabd_glycop.
Pfam; Pr00974; Rhabd_glycop; 1.
Transmembrane; Envelope protein; Glycoprotein; Signal.
                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
50S ribosomal protein L32.
   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-83138980; PubMed-6298453;
                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequ
                                                                                                                                                                                                                          Spike glycoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58229 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; V01214; CAA24525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.38;
   Conservative
                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517
179
340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 3
517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRUS BUDDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11283;
                                                              299 CKGGVC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 CKGQIC 174
                             1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPMF OR TC0195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CKGAIC 6
   4
                                                                                                                                          VGLG_VSVJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RL32_CHLMU
Q9PLB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                            VGLG_VSVJO
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                              RESULT 4
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                                                                         STRAIN-MOPN / Nigg;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Atriplex. NCBL_TaxID=35922;
                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cairney J., Newton R.J., Funkhouser E.A., Chang S., Hayes D.;
"Nucleotide sequence of a cDNA for a water channel protein
(aquaporin) homolog from Atriplex canescens (Pursh.) Nutt.";
Plant Physiol. 108:1291-1292(1995).
-! FUNCTION: WATER SPECIFIC CHANNEL.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AA; 6379 MW; F9D8F77C8730B29D CRC64;
  Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 1;
Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002677; Ribosomal_L32p.
Pfam; PF01783; Ribosomal_L32p; 1.
IGRFAMs; IGR01031; rpmr_bact; 1.
Ribosomal protein; Complete BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-PURSH NUTT;
MEDLINE-95357416; PubMed-7543207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE002286; AAF39069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atriplex canescens (Saltbush).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                  NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 CSGAVC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQUA_ATRCA
P42767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aquaporin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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qq
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"Catabolism of phenylacetic acid in Escherichia coli. Characterization of a new aerobic hybrid pathway.";
J Biol. Chem. 273:25974-25986(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH TRYPSIN (BY SIMILARITY). INTERACTION WITH CHYMOTRYPSIN (BY
                                                                                                                                                                                                                                                                   Funk A., Weder J.K., Belitz H.-D.;
Funk A., Weder J.K., Belitz H.-D.;
Primary structures of proteinase inhibitors from Phaseolus vulgaris
var. nanus (cv. Borlotto).".
Z. Lebensam. Unters. Forsch. 196:343-350(1993).
--- SIMILARITY: BELONGS TO THE BOWMAN-BIRK SERINE PROTEASE INHIBITORS
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
16-MIN-2002 (Rel. 41, Last amnotation update)
16-MIN-2002 (Rel. 41, Last amnotation update)
16-MIN-2002 (Ridney bean) (French bean)
16-MIN-2002 (Ridney bean) (French bean)
17-MIN-2004 (Ridney bean) (French bean)
17-MIN-2004 (Ridney bean)
17-MIN-2004 (Ridney bean)
17-MIN-2004 (Ridney bean)
18-MIN-2004 (Ridney bean)
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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STAILN-HIZ / MGIBSS;
MEDIINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARE_ECOLI STANDARD; PRT; 356 AA.
P76081; 053013; P77233;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable phenylacetic acid degradation NADH oxidoreductase paaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
BY SIMILARITY.
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOWMAN_BIRK; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01055; 1BB1.
InterPro; IPR000877; Bowman-Birk_leg.
Pfam; PF00228; Bowman-Birk_leg; 1.
ProDom; P000168; Bowman-Birk_leg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98421522; PubMed=9748275;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9231 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease inhibitor.
ACT_SITE 30 31
ACT_SITE 57 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=W / ATCC 11105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00269; BOWB;
PROSITE; PS00281; BOWN
                                                                                                                                                                                                                                                        Borlotto;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                             NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKGAIC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20229831; PubMed-10766858; Retrandez A. Garcia V.L., Diaz E.; Ferrandez A., Garcia V.L., Diaz E.; Transcriptional regulation of the divergent paa catabolic operons for phenylacetic acid degradation in Escherichia coli."; J. Biol. Chen. 275:1214-12222(2000).
-: FUNCTION: MAY BE PART OF A MULTICOMPONENT OXYGENASE INVOLVED IN PHENYLACETYL-COA HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLAYOPROTEIN OXIDOREDUCTASES FAMILY.
-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE 2FE2S PLANT-TYPE FERREDOXIN FAMILY.
                                                                                                                                                                                                                                                                             Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Maki T., Mizobuchi K., Mori T., Motomura K., Makide S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takeuchi Y., Moriuchi Y., Moriuchi Y., Moriuchi Y., Wada C., Yamamoto Y., Moriuchi T., Takeuchi Y., Wali Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEREEDOXIN (POTENTIAL).
IRON-SULEUR (2FE-2S) (BY SIMILARITY).
IRON-SULEUR (2FE-2S) (BY SIMILARITY).
IRON-SULEUR (2FE-2S) (BY SIMILARITY).
IRON-SULEUR (2FE-2S) (BY SIMILARITY).
S -> P (IN STRAIN W).
P -> S (IN STRAIN W).
DAET -> ETEA (IN STRAIN W).
MM, D719C1CA81DA5FFA CRC64;
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- COFACTOR: FAD AND A 2FE-2S CLUSTER (BY SIMILARITY).
-i- PATHWAY: Phenylacetic acid aerobic catabolism.
-i- INDOCTION: ACTIVATED BY CAMP RECEPTOR PROTEIN (CRP) AND INTEGRATION HOST FACTOR (IHF). INHIBITED BY PAAX.
-i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 356;
                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXIDOREDUCTASE (POTENTIAL).
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Pfam; PF00970; RAD_binding=6; 1.
PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
Oxidoreductase; Flavoprotein; FAD; NAD; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB Pred. No. 24;
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EMBL; AE000236; AAC74474.1; -...
EMBL; D90777; BAA14998.1; ALT_INIT.
HSSP; P06543; 1J7B.
EcoGene; EG13739; paaE.
InterPro; IPR001834; CYLBS_reductase.
InterPro; IPR001834; CYLBS_reductase.
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112892 seqs, 41476328 residues Searched:

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SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | | P81484 phaseolus v | | _ | | _ | P42767 atriplex ca | aeropyrum | | | mus m | Q99965 homo sapien | metha | | arabidopsi | P30302 arabidopsis | lycopersic | P43285 arabidopsis | | | arabidopsi | | 0.0 | 9 | 14 | 24 | Q9z899 chlamydia p | 54 mus muscul | 0 | | 86 | 338 mus | Q07120 rattus norv | 786 homo s |
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| | ID | | IBB3_PHAVU | IBB4_PHAVU | PAAE_ECOLI | VGLG_VSVJO | RL32_CHLMU | AQUA_ATRCA | LIPA_AERPE | C43B_BOVIN | C43B_HUMAN | C43B_MOUSE | AD02_HUMAN | FER4_METJA | PA21_ACAAN | WC2B_ARATH | WC2C_ARATH | TIPW_LYCES | WC1A_ARATH | WC1B_ARATH | WC1C_ARATH | WC2A_ARATH | YF34_SYNY3 | - 1 | ADH1_RANPE | YP65_CAEEL | - 1 | - 1 | - 1 | VGF1_IBVB | CYC3_DESGI | VIEL_FRG3V | - 1 | GFI1_RAT | TFR1_HUMAN |
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| | Length | | 82 | 82 | 356 | 517 | 28 | 282 | 295 | 624 | 624 | 624 | 735 | 62 | 119 | 282 | 282 | 286 | 286 | 286 | 286 | 287 | 301 | 323 | 375 | 7.29 | 870 | 1276 | 2871 | 3951 | 112 | 157 | 423 | 423 | 760 |
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PRT; * 85 AA.

RESULT 2 IBB4_PHAVU ID IBB4_PHAVU STANDARD; P AC P81483; DT 15-DEC-1998 (Rel. 37, Created)

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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basul A., Rarendale J., Bardskraroglu L., Beasley E.M.,
RA Ballew R.M., Basul A., Barcandale J., Bandario D., Bollahakov S.,
Benkova D., Borchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Borchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrac C., Ferrac C., Ferrac C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Burtis N.J., Boutory D., Helman T.J., Herrandez J.R., Plouck J.,
RA Harris N.L., Harvey D., Helman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Houston K.A., Howland T.S., Wei M.-H., Ibegram C.,
RA Jalali M., Kalush F., Karft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lel Y., Levitsky A.A.,
Liu X., Mattei B., McInton T.G., Morris J., Moshrefi A.,
Raisch D.R., Nelson R.A., Howland T.S., Weiseler F., Shen H.,
Raisch D.R., Nelson R.A., Mixon K., Musskern D.R., Pacleb J.M.
Raischlor G. Milshina N.V., Mobarry C., Morris J., Wolfer F., Sanh T.,
Raiscon D.R., Nelson R.A., Nixon K., Watskern D.R., Pacleb J.M.
Raiscon D.R., Remington K.A., Nixon K., Wutskern D.R., Pacleb J.M.
Raiscon D.R., Wassaman D.A., Mainstock G. M., Welsenberd J.,
Raiscon D.R., Woodage T., Simpson M., Strong S., Zho Q., X.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q., A.,
Raiscon S., Raisconder S., Raisconder S., Shang S., Polland S., Pacle S., P
                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                 EG:140G11.3 protein.
EG:140G11.3 OR CG4015 OR CG18508.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY
                                                                                             51 CKGGVC 56
                                                   1 CKGAIC 6
         4;
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                                                                                                                                                              RESULT 15
097172
         Matches
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-GEV-VG;
GG Y., YOU Y., XU Q.;
"Analysis of the major open reading frames' nucleotide sequences in GOOSE parvovirus GPV-YG strain isolated in China.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IFFR001257; Parvo. NSI.
Pfam; PF01057; Parvo. NSI.
SEQUENCE 627 AA; 71943 MW; 4301A125FCACA7DI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronniller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   goose parvovirus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                   Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 5; Length 69; Pred. No. 10;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY071325; AAL48947.1; -. SEQUENCE 69 AA: 8120 MW; F5CE3B840B3DAB7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157; Parvo_NS1; 1.
627 Aa; 71943 MW; 4301A125FCACA7D1 CRC64;
    71928 MW; C909B8878B1AC0F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F5CE3B840B3DAB7F CRC64;
                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                          ;
                                                   DB 12;
                                                                                                                                                                                                                                                                                            627 AA.
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                                         89.2%; Score 33; DB 66.7%; Pred. No. 41; ive 2; Mismatches
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                    Query Match
Best Local Similarity 66./*,
A: Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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627 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=38251;
                                                                                                                                                                              407 CKGSVC 412
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                                                                                                                                    1 CKGAIC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKGAIC 6
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Q8SYT4;

Q8SYT4

RESULT 14 Q8SYT4

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STRAIN-FM;
     Query Match
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Q67665;
                                                                                                                                      065443
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Matches
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"Evidence for sulfate derepression of an arylsulfatase gene of
"Evidence for sulfate derepression of an arylsulfatase gene of
Colletotrichum gloeosporioides f.sp. malvae during infection of round-
leaved mallow, Malva pusilia.";
Physiol. Mol. Plant Pathol. 57:169-176(2000).
EMBL; AJ71152; CAB70953.1;
InterPro; IPR000917; Sulfatase.
PFam; PF00884; Sulfatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                              Colletotrichum gloeosporioides f. sp. malvae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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NCBL_TaxID=37325;
                                                                                                  ó
                                                                        89.2%; Score 33; DB 12; Length 461; 66.7%; Pred. No. 32; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.2%; Score 33; DB 3; Length 511; 66.7%; Pred. No. 35; 1. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zadori Z., Erdei J., Nagy J., Kisari J.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X75033, CAA52983.1; -.
InterPro; IPRO1257; Parvo.NS1.
Pfam; PF01057; Parvo.NS1.
SEQUENCE 626 AA; 71683 MW; 0A088CA3B0F5CBCI CRC64;
EMBL; U34761; AAA75285.1; -.
InterPro; IPR001257; Parvo_NS1.
Pfam, PF01057; Parvo_NS1; 1.
NON_TER 1 1
SEQUENCE 461 AA; 52594 MW; 7D07F2672EB834EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1
SEQUENCE 511 AA; 57405 MW; E9AC0739E3E0D69B CRC64;
                                                                                                                                                                                                                                01-071-2000 (TrEMBLrel. 15, Created)
01-071-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Arylsulfatase (EC 3.1.6.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.77
Conservative
                                                                                    Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muscovy duck parvovirus.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=96478;
                                                                                                                                        |||::|
241 CKGSVC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CKGAIC 6
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                                                                           Query Match
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                                                                                                                                                                                                            Q9P8C2
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Q83288
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Q9P8C2
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Gaps
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Zadori Z., Stefancsik R., Rauch T., Kisary J.;
Zadori Z., Stefancsik R., Rauch T., Kisary J.;
"Analysis of the complete nucleotide sequences of goose and muscovy
duck parvoviruses indicates common ancestral origin with adeno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96010229; PubMed-7571426; Zadori Z., Stefancsik R., Rauch T., Kisary J.; Analysis of the complete nuclectide sequences of goose and muscovy duck parvoviruses indicates common ancestral origin with adeno-
                                                                                                                                                                                                                                                                                                                    Barbarie duck parvovirus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBL_TaxID=39118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     goose parvovirus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=38251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 89.2%; Score 33; DB 12; Length 627; Local Similarity 66.7%; Pred. No. 41; es 4; Conservative 2; Mismatches 0; Indels
89.2%; Score 33; DB 12; Length 626; 66.7%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 025749; AAA83229.1; -.
InterPro: IPRO1257; Parvo_NS1.
Pfam; PF01057; Parvo_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Associated virus 2.7;
Virology 212:562-573(1995).
EMBL; U2267; AAA83224.1; -.
InterPro; IPROU1257; Parvo_NS1.
SEQUENCE 627 AA; 71812 MW; C359097CDDA967DC CRC64;
                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
REP protein.
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Last annotation update)
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                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 212:562-573(1995).
                 Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                             406 CKGSVC 411
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                                                                      1 CKGAIC 6
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89.2%; Score 33; DB 2; Length 270; 83.3%; Pred. No. 20;

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Pfam; PF01149; Fapy_DNA_glyco; 1.
ProDom; PD003680; Fapy_DNA_glyco; 1.
TIGRRAMS; TIGR00577; fpg; 1.
SEQUENCE 270 AA; 30736 MW; 44B3306AF754DDB CRC64;
                                                                                                                                            Best Local Similarity
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MEDLINE=20446260; PubMed=10988064;
Beja O., Aravind L., Koonin E.V., Suzuki M.T., Hadd A., Nguyen L.P.,
Jovanovich S.B., Gates C.M., Feldman R.A., Spudich J.L., Spudich E.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AT19932p.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stappeton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Erise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mingall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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"Bacterial rhodopsin: evidence for a new type of phototrophy in the
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                                                                                                                                                                                                                  1; Indels
                     German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A1356834; CAB2713.2; -.
Hypothetical protein.
SEQUENCE 137 AA; 14743 MW; 35FF23569D4616AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY075239; AAL68106.1; --
SEQUENCE 260 AA; 29048 MW; A254A62E23471A51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
predicted formamidopyrimidine-DNA glycosylase.
uncultured protecobacterium EBAC31A08.
Bacteria; Proteobacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                0; Mismatches
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EMBL; AF279106; AAG10477.1; -.
HSSP; O50606; 1EE8.
InterPro; IPR000191; Fapy_DNA_glyco.
                                                                                                                                                                  89.2%;
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les 4; Conservative
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                        93 CKGGIC 98
                                                                                                                                                                                                                                                           1 CKGAIC 6
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Celniker S.;
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09F79
1D 09F71
1D 09F71
1D 09F71
1D 01-M
1D 0
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Gaps
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MEDLINE=55343541; PubMed=7618268;
Brown K.E., Green S.W., Young N.S.;
Goose parvovirus--an autonomous member of the dependovirus genus?";
Virology 210:283-291(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=GB-MI;
STRAIN=GB-MI;
MEDLINE=21576510; PubMed=11719806;
MEDLINE=21576510; PubMed=11719806;
Factinka M.D., Duprat S., Cornillot E., Metenler G., Thomarat F.,
Frensler G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
mature 414.450-453(2001).
EMBL; AL590443; CAD25255.1;
EMBL; AL590441; CAD27073.1; -.
SEQUENCE 383 AA; 42475 MW; 677047CE70BC118D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              goose parvovirus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
  1; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                       383 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.2%; Score 33; DB 66.7%; Pred. No. 27; Live 2; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                       PRT;
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Best Local Similarity 66./~
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                60S ribosomal protein L3. ECU03_1220 OR ECU09_1000. Encephalitozoon cuniculi.
  5; Conservative
                                                                                                                                                                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                        111 11
248 CKGTIC 253
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                                              1 CKGAIC 6
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Q8SQI3
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Q67671
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NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The precursor region of a protein active in sperm-egg fusion contains a metalloprotease and a disintegrin domain: Structural, functional, and evolutionary implications.", Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1993).
                                                                                                                                                                                                                                                                                         A potential fusion peptide and an integrin ligand domain in a protein active in sperm-egg fusion.";
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                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=TESTIS;
Wolfsberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,
White J.M.;
                                                                                                                                                                                                                             MEDLINE-92204234; PubMed-1552944;
Blobel C.P., Wolfsberg T.G., Turck C.W., Myles D.G., Primakoff P.,
  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Guinea pig PH-30 beta precursor.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PH-30 PRO-BETA FOUND ON TESTICULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPERMATOGENIC CELLS.
MATURE PH-30 BETA PRESENT ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolfsberg T.G.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; 211720; CAA7784.1; -.
HSSP; P18619; IFVL.
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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1; Mismatches
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AC 09LQT3.

DT 01-CCT-2000 (TrEMBLrel. 15, Created)

DT 01-ONY-2001 (TrEMBLrel. 15, Last sequen

DT 01-JNY-2001 (TrEMBLrel. 17, Last annota

DF 14-012.4.

St_marabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN_1; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam. PF00200; disintegrin; 1. Pfam. PF01562; Pep_M12B_propep; 1. Pfam; PF01421; Reprolysin; 1. ProDom; PD000664; Disintegrin; 1.
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SMART; SM00181; EGF; 1.
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                                                                                                                                                                                                                                                                                                                   active in sperm-egg fusio
Nature 356:248-252(1992).
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735
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                                                                                                                                                     NCBI_TaxID=10141;
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16
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chaou J., Choi E.,

Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

Conn I., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,

Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,

Theologis A., Ecker J.;
                                                                                                                                                                                                                                          Chao O., Shinn P., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Walker M., Brooks S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Towley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.; "Genomic sequence for Arabidopsis thaliana BAC 74012 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecker J.R.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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01-0cr-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-1001 (TremBLrel. 19, Last annotation update)
B11822.100.
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Best Local Similarity
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(without alignments)
77.641 Million cell updates/sec
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                                                                                         November 9, 2002, 13:59:04; Search time 15.9231 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                           OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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Maximum DB seq length: 200000000
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!: sp_archea:*
!: sp_bacteria:*
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37
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sp_rodent:*
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Match Length DB
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Perfect score:
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Q9f7p2 uncultured Q8sqi3 encephalito Q67671 goose parvo Q9p8c2 colletotric 082288 muscovy duc 066443 barbarie du 067665 goose parvo 08v396 goose parvo 08sy14 drosophila 097172 drosophila 08yek7 brucella me Q60411 cavia porce Q91qt3 arabidopsis Q9p4y2 neurospora Q8t8w9 drosophila Q8zyu8 pyrobaculum Q60411 cav1a porce Q8T8W9 Q9F7P2 Q8SQI3 Q67671 Q9LQT3 Q9P4Y2 Q9P8C2 Q83288 Q82YU8 Q60411 Q65443 Q67665 O97172 Q8YEK7 **08V**396

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PRELIMINARY;

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RESULT 2 Q60411 ID Q6041 AC Q6041

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| | Q84947 vesicular s Q84573 ralstonia s Q9351c1 streptomyce Q9xzz8 litcomosoide Q96668 home sapien Q96491 vesicular s Q96475 vesicular s Q89007 vesicular s Q89007 vesicular s Q89010 vesicular s Q89011 vesicular s Q89011 vesicular s Q89012 vesicular s Q89013 vesicular s Q89013 vesicular s Q89013 vesicular s Q89014 vesicular s Q89016 vesicular s Q89017 vesicular s Q89016 vesicular s Q89017 vesicular s Q89016 vesicular s Q89017 vesicular s | AA.
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on update) | . Thermoproteales; | .m UJ., Stetter K.O., Simon M.I., ermophilic crenarchaeon Pyrobaculum 9:984-989(2002). Proteome. C5822D009DFF808C CRC54; |
|--------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|
| 091G71
091G68
091G64
091G65
091G55
091G57
091G53 | 09164/
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099609/
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UB VB | PAEG613. Pyrobaculum aerop Archaea, Crenarch Thermoproteaceae; NCBI_TaxID=13773; [1] SEQUENCE FROM N.A STRAIN-IM2 / ATCC | SOFE EX |
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RN [1] | |

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Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009775; AALG2895.1; -
Hypothetical protein; Complete protecme.
SEQUENCE 221 AA; 24620 MW; C5822D009DFF808C CRC64;
                                                                                                                                                                                                                                                                                                                                          Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.6%; Score 35; DB 17; Length 221; 83.3%; Pred. No. 6.1; 1ive 1; Mismatches 0; Indels
                                                                                                                         Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteacese; Thermoproteacese; Pyrobaculum.
NCBI_TaxID=13773;
vi-wak-2002 (TEMBLrel. 20, Created)
01-MAR-2002 (TEMBLrel. 20, Last sequence update)
1-MAR-2002 (TEMBLrel. 20, Last annotation update)
Hypothetical protein PAE0613.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed-11792869;
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Matches 5; Conserv
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| 157 CKGALC 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATIVE PETSON, et al.
TITLE OF INVENTION: Multifunctional Neurotrophic Factors
WIMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.6%; Score 34; DB 1; Length 120; Best Local Similarity 87.5%; Pred. No. 31; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIONS SOFTWAN FOR SOFTWAN FOR SOFTWAN APPLICATION DATA:
APPLICATION NUMBER: US/07/979,630
FILING DATE: 20-NOV-1992
CLASSIFICATION 1300
PRIOR APPLICATION NUMBER: US 07/847,369
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kempler Ph.D., Gail M.
REGISTRATION NUMBER: 32,143
REGISTRATION NUMBER: 32,143
RELECOMMUNICATION INFORMATION:
TELEPHONE: 914-347-7000
TELEPAX: 914-347-2113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TELEFAX: (415) 494-0792
TELEX: 706141 MRSWFDERS SFO
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07979630 Patent No. 5488099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                  // MOLECULE TYPE: protein US-08-753-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 10591
COMPUTER READABLE FORM:
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29 ATDIKGKE 36
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28 ATDIKGKE 35
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US-07-979-630-1
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Search completed: November 9, 2002, 14:04:23

Job time : 14.0769 secs

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APPLICANT: Persson, Hakan B. et al.
TITLE OF INVENTION: Neurotrophic Factors Having Altered
TITLE OF INVENTION: Receptor Binding Specificities
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
59.6%; Score 34; DB 1; Length 12; 87.5%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 12;
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                                                                                                                                                                                                                                          Neurotrophic Factors Having Altered
Receptor Binding Specificities
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Regeneron Pharmaceuticals, Inc. STRRET: 777 Old Saw Mill River Road CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kempler, Gail M./Misrock, S. Leslie
REGISTRATION NUMBER: 32,143/18,872
REFERENCE/DOCKET NUMBER: 6526-097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regeneron Pharmaceuticals, Inc
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Pred. No. 3;
0; Mismatches
                               0; Mismatches
                                                                                                                                                                                                                         APPLICANT: Persson, Hakan B. et al. TITLE OF INVENTION: Neurotrophic FaTITLE OF INVENTION: Receptor Bindin
                                                                                                                                                                         Sequence 1, Application US/08300044 Patent No. 5705617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08300044
Patent No. 5705617
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TELEPHONE: 914 347-7000
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INFORMATION FOR SEQ ID NO: 1:
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87.58;
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LENGTH: 12 amino acids
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Best Local Similarity 87.5.
               Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
                                                                                  ||||||| |
4 ATDIKGKE 11
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                                                                                                                                                           US-08-300-044-1
   Query Match
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TITLE OF INVENTION: WOUND TREATMENT METHOD WITH NERVE GROWTH
TITLE OF INVENTION: FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.6%; Score 34; DB 1; Length 12; ilarity 87.5%; Pred. No. 3; Conservative 0; Mismatches 1; Indels
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APPLICATION NUMBER: US/08/753,642
FILING DATE: 27-NOV-1996
CLASSIFICATION: 514
TATORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/300,044
FILLING DATE: US-08/300,044
FILLING DATE: US-08/300,044
CLASSIFICATION NUMBER: US/08/300,044
APPLICATION NUMBER: US/08/47,369
FILLING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
RESISTRATION NUMBER: 32,143/18,872
REFERENCE/DOCKET NUMBER: 6526-097
TELEPHONE: 914 347-7000
TELEPHONE: 914 347-7000
    777 Old Saw Mill River Road
STREET: 777 Old Saw Mill River Roa CITY: Tarrytown STARE: New York COUNTRY: U.S.A. 2.P. 10591-6707 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OF POSYMEN: PC-DOS/MS-DOSYMENTORY SYSTEM: PC-DOS/MS-DOS/MS-DOSYMENTORY SYSTEM: PC-DOS/MS-DOSYMENTORY S
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08753642
Patent No. 6063757
GENERAL INFORMATION:
APPLICANT: URSO, RICHARD G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 914 347-2113
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-300-044-2
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 777 Old SCITY: Tarrytown STATE: New York COUNTRY: U.S.A. ZIP: 10591-6707
                                                                                                                                                                                                      FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ATDIKGAE 9
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OTHER INFORMATION: /note= "Xaa is any uncharged amino acid
OTHER INFORMATION: or hydropathic amino acid"
                                        NERVE GROWTH FACTOR STRUCTURAL ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07847369
Patent No. 5349055
GENERAL INFORMATION:
APPLICANT: Persson, Hakan B. et al.
TITLE OF INVENTION: Neurotrophic Factors Having Altered TITLE OF INVENTION: Receptor Binding Specificities
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.6%; Score 34; DB 3; Length 10;
85.7%; Pred. No. 2.5;
tive 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIBER: US/08/696,854B
FILING DATE: 07-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA95/00059
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9402331.4
FILING DATE: 07-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          ADDRESSEE: KLAUBER & JACKSON
STREET: Continental Plaza, 411 Hackensack Avenue
CITY: Hackensack
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STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: US.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
                                                                            AND THEIR USES
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APPLICANT: CUELLO, Claudio A. TITLE OF INVENTION: NERVE GRO TITLE OF INVENTION: AND THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
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Matches 6; Conservative
                                                                                                             NUMBER OF SEQUENCES: 23
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                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10 amino
TYPE: amino acid
STRANDEDNESS: Sin
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3 DIKGKEC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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OCHAPTER: THEN PC conceptible
SOCTAMENT PRESENT POTOSYSTEM
CURRENT APPLICATION DATA:
SOCTAMENT PATENTION DATA:
SOCTAMENT PATENTION DATA:
CURRENT APPLICATION NUMBER:
SOCTAMENT PATENTION DATA:
APPLICATION NUMBER:
SOCTAMENT PATENTION PATENTIAL
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us-09-632-748-9.rai

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Score 34.5; DB 4; Length 1296;
Pred. No. 2.8e+02;
1; Mismatches 2; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,854B
FILING DATE: 07-AUG-1996
PRIOR APPLICATION NUMBER: WO-PCT/CA95/00059
FILING DATE: 07-REB-1995
FILING DATE: 07-FEB-1995
PRIOR APPLICATION NUMBER: GB 9402331.4
FILING DATE: 07-FEB-1994
ATPRICATION NUMBER: GB 9402331.4
FILING DATE: 07-FEB-1994
ATPRICATION NUMBER: GB 9402331.4
FILING DATE: 07-FEB-1994
ATPRICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: KLAUBER & JACKSON
Continental Plaza, 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                        US-08-696-854B-5; Sequence 5, Application US/08696854B; Patent No. 6017878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 487-5800
TELEFAX: (201) 343-1684
                 60.5%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 8/...
And 7; Conservative
Query Match
Best Local Similarity 53.0.
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                                                                                                                                           1006 CVTLGIDVKGAAC 1018
                                                                                                    1 CAT---DIKGAEC 10
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hackensack
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1 ATDIKGKE 8
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TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease
FILE REFERENCE: 4239-53894
CURRENT APPLICATION NUMBER: US/09/462,136
CURRENT FILING DATE: 2000-06-01
PRIOR PILING DATE: 1998-07-03
PRIOR FILING DATE: 1998-07-03
PRIOR FILING DATE: 1997-07-03
PRIOR FILING DATE: 1997-07-03
NUMBER: PATENTION NUMBER: US 60/051,682
PRIOR FILING DATE: 1997-07-03
SOFTWARE: PATENTIN VORT: 13
SOFTWARE: PATENTIN VORT: 2.0
SEQ ID NO 9
LENGTH: 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1124;
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06093
FILING DATE: 19930625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.4%; Score 35; DB 5; 1
60.0%; Pred. No. 1.9e+02;
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                                                                                                       APPLICANT: Ziegler, Steven F.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/905,600 FILING DATE: 26-UN-1992 ATTORNEY/AGENT INFORMATION: NAME: Seese, Kathryn A. REGISTRATION NUMBER: 32,172 REGISTRATION NUMBER: 32,172 RECECOMMUNICATION INFORMATION: TELECOMMUNICATION 1005 33-0644 TELEX: 756822 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1124 amino acids: TTPE: AMINO ACID
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                            Sequence 2, Application PC/TUS9306093 GENERAL INFORMATION:
                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-462-136-9; Sequence 9, Application US/09462136; Patent No. 6426198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein PCT-US93-06093-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19930625
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
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                                          PCT-US93-06093-2
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3;
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APPLICANT: LESAUTEDR. Lynne
APPLICANT: CUELLO, Claudio A.
TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
TITLE OF INVENTION: AND THEIR USES
CORRESPONDENCE: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
UG-08-696-854B-2
; Sequence 2, Application US/08696854B
; Patent No. 6017878
; GENERAL INFORMATION:
; APPLICANT: SARAGOVI, Uri H.
APPLICANT: LESAUTEUR, LYONE
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Gaps

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61.4%; Score 35; DB 4; Length 977; 60.0%; Pred. No. 1.7e+02; tive 1; Mismatches 3; Indels

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CURRENT APPLICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/137,889
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ. ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                          Best_Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      1 CATDIKGAEC 10
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                                                                                                                        SEQ ID NO 1
LENGTH: 977
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US-08-323-474-2
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                                                                                                                                                                                                    us-09-590-656-1
                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: 01, Huilin
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
FILE REFERENCE: 7326-046
CURRENT APPLICATION NUMBER: US/08/899,232
CURRENT FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.2e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-590-656-2
Sequence 2, Application US/09590656
Setent No. 641393
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
APPLICANT: BOTGES, Luis G.
APPLICANT: Fanslow, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT FILING DATE: 2000-6-07
PRIOR PELICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 2000-6-07
PRIOR FILING DATE: 1999-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09590656; Patent No. 6413922; GBNERAL INFORMATION: APPLICANT: Cerretti, Douglas P. APPLICANT: Borges, Luis G. APPLICANT: FRAISLOW. III, William C. TITLE OF INVENTION: TEK ANTAGONISTS; FILE REFERENCE: 2900-A.
                                                                                  RESULT 2
US-08-899-232-4
; Sequence 4, Application US/08899232
; Patent No. 6436550
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60.0%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 704
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Best Local Similarity 60.0
Matches 6; Conservative
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CORGANISM: Drosophila sp.
US-08-899-232-4
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289 CATGWKGLQC 298
          ||| || :|
437 CATGYKGVDC 446
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Matches 6; Conserv
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US-09-590-656-1
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,474
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: 21egler, Steven F.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
CITY: Seattle
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION, NUMBER: US 07/905,600
FILING DATE: 26-U0M-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELEPOWNUICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFRA (206) 233-0644
TELER: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                   Sequence 2, Application US/08323474 Patent No. 5447860
                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1124 amino acids
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Best Local Similarity
Matches 6; Conserva
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289 CATGWKGLQC 298
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289 CATGWKGLQC 298
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APPIII
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                                                                                                                                                                    9, 2002, 13:59:59; Search time 13.0769 Seconds (without alignments) 22.500 Million cell updates/sec
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Sequence 3,
Sequence 31
Sequence 2,
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-185-432-19
US-08-899-232-4
US-09-590-656-2
US-09-590-656-1
US-08-323-474-2
US-09-462-18-2
US-09-462-18-2
US-09-462-18-2
US-08-847-369-1
US-08-847-369-1
US-08-847-369-1
US-08-18-2
US-08-18-2
US-08-18-2
US-08-18-2
US-08-44-513A-1
US-08-441-513A-3
US-08-441-513A-3
US-08-970-865-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-845-541B-4
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Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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57
1 CATDIKGAEC 10
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Match Length
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Perfect score:
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Appli
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APPLICANT: Busseau, Isabelle
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
APPLICANT: Matsuno, Kenji
APPLICANT: Matsuno, Kenji
APPLICANT: Matsuno, Renji
APPLICANT: AND COMPOSITIONS
NUMBER OF SEQUENCES: 2
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                            Sequence 3, P
Sequence 4, P
Sequence 5, P
Sequence 7, P
Sequence 8, P
                                                                                                                                                                                                                                                                                                                        Sequence 10,
                                                                              Sequence 1
Sequence 1
Sequence 1
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Sequence 1
Sequence 2
                                                                                                                                                                                         Sequence
                                          Sequence
                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
US-08-845-5418-7
US-08-845-5418-7
US-08-845-5418-18
US-08-845-5418-11
US-08-845-5418-12
US-08-845-5418-12
US-08-845-5418-13
US-08-845-5418-19
US-08-845-5418-20
US-08-845-5418-21
US-08-845-5418-21
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-3
US-09-066-065A-7
US-09-066-065A-7
US-09-066-065A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-185-432-19; Sequence 19, Application US/08185432 petent No. 5750652; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2703 amino acids
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   RESULT 1
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Gaps

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Score 38; DB 1; Length 2703; Pred. No. 1.4e+02; 1; Mismatches 3; Indels

Similarity 60.0%; 6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

US-08-185-432-19

1 CATDIKGAEC 10

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                                                                                                                                       Sequence 6, Application US/09305856B

Sequence 6, Application US/09305856B

Patent No. US20020061518A1

GENERAL INFORMATION:
APPLICANT: Penny, Laura

TITLE OF INVENTION: Genotyping the Human
TITLE OF INVENTION: UDP-Glucuronosyltransferase 1 (UGTL) Gene
FILE REFERENCE: 1999-05-05

CURRENT APPLICATION NUMBER: US/09/305,856B

CURRENT APPLICATION NUMBER: US/09/305,856B

PRIOR FILING DATE: 1999-05-05

PRIOR FILING DATE: 1999-05-07

NUMBER OF SEQ ID NOS: 124

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penny, Laura
APPLICANT: Galvin, Margaret
TITLE OF INVENTION: Genotyping the Human
TITLE OF INVENTION: Genotyping the Human
TITLE OF INVENTION: UDD-Glucuronosyltransferase 1 (UGT1) Gene
FILE REFERENCE: 4389-7 (formerly SEQ-17CIP)
CURRENT PAPLICATION NUMBER: US/09/305,8568
CURRENT FILING DATE: 1990-05-05
PRIOR APPLICATION NUMBER: 60/084,807
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENTH: 289
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US-09-919-497-53
Sequence 53, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 8, Application US/09305856B
; Patent No. US20020061518A1
; GENERAL INFORMATION:
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Best Local Similarity 50.03
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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US-09-305-856B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                          178 CDLDFKGTQC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 CDLDFKGTQC 187
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1 CATDIKGAEC 10
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US-09-305-856B-8
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; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER; FILE REFERENCE: B0801/7225.
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR RILING DATE: 2000-07-31
; PRIOR RILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
; SOFTWARE: PAT
; ORGANISM: Homo sapiens
US-09-919-497-53

QUETY MATCh
Best Local Similarity 55.6%; Pred. No. 32;
MATChes 5; Conservative 2; Mismatches 2; Indels 0; Gaps
QY 1 CATDIRGLE 159

Search completed: November 9, 2002, 14:11:55
JOB 151 CCTDLRGLE 159

Search completed: November 9, 2002, 14:11:55
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